

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:03:48 ; Search time 30.82 Seconds
(without alignments)
1571.934 Million cell updates/sec

Title: US-09-692-504-1
Perfect score: 3498
Sequence: 1 MRGGRGAPFWLPLPKALL.....FLPTPEELGLGPPRPQVLA 636
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3498	100.0	636	2 JH0047	class I cytokinase
2	298.5	8.5	783	2 JH0329	granulocyte colony
3	292	8.3	863	2 C38252	granulocyte colony
4	277	7.9	837	2 A34898	granulocyte colony
5	268.5	7.7	771	2 B38252	granulocyte colony
6	250	7.1	918	2 A36337	membrane glycoprot
7	248	7.1	917	2 I49699	glycoprotein 130 -
8	226.5	6.5	918	2 A44257	interleukin-130
9	206.5	5.9	1097	2 S17308	leukemia inhibitor
10	206	5.9	1092	2 JX0312	differentiation-st
11	178	5.1	894	1 A41527	protein-tyrosine k
12	170	4.9	1711	1 A55148	protein-tyrosine k
13	164.5	4.7	1185	2 T46428	hypothetical prote
14	162.5	4.6	1197	2 T30581	neural cell adhesi
15	159	4.5	1825	2 T32828	hypothetical prote
16	155	4.4	942	2 S3251	protein-tyrosine k
17	154.5	4.4	880	2 S33743	protein-tyrosine k
18	151	4.3	1274	2 S55050	cardiac myosin-bin
19	151	4.3	1914	2 T42635	tenascin Y precurs
20	150	4.3	888	2 S23065	ufo protein -mous
21	150	4.3	1232	2 T43027	neural cell adhesi
22	147.5	4.2	800	1 S31575	interleukin-4 rece
23	147.5	4.2	1239	1 A32579	neuroglian - fruit
24	146	4.2	876	2 I49152	protein-tyrosine k
25	146	4.2	1691	1 D54689	protein-tyrosine-p
26	144	4.1	890	1 A53743	protein-tyrosine k
27	144	4.1	1894	2 C54689	protein-tyrosine-p
28	143.5	4.1	4135	2 T42629	tenascin-X - bovin
29	142.5	4.1	1898	2 S46216	leukocyte antigen-

ALIGNMENTS

RESULT 1

JW0047

class I cytokinase receptor precursor - human

N:Alternate names: WSX-1

C:Species: Homo sapiens (man)

C>Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000

C:Accession: JW0047

R:Spencer, C.A.; Grant, F.J.; Baumgartner, J.W.; Presnell, S.R.; Schrader, S.K.; Yam

Biochem. Biophys. Res. Commun. 246, 82-90, 1998

A:Title: Cloning and characterization of a novel class I cytokine receptor.

A:Reference number: JW0047; MUID:98262921

A:Accession: JW0047

A:Molecule type: mRNA

A:Residues: 1-836 <SPR>

A:Cross-references: GB:AF053004; NID:g3153240; PIDN:AAC39755.1; PID:g3153241

A:Experimental source: brain

C:Genetics:

A:Map position: 19p13.11

C:Keywords: glycoprotein

F:1-32/Domain: signal sequence #status predicted <SIG>

F:515-540/Domain: transmembrane #status predicted <TM>

F:554-561/Domain: cytoplasmic #status predicted <CTP>

F:51.76.302.311.374.382.467/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 100.0%; Score 3498; DB 2; Length 636;

Best Local Similarity 100.0%; Pred. No. 1.7e-231;

Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRGGRGAPFWLPLPKALLPLLWLFTQTRPQGSAGPLQCYGVGLDNCWEPLGDL 60

Db 1 MRGGRGAPFWLPLPKALLPLLWLFTQTRPQGSAGPLQCYGVGLDNCWEPLGDL 60

Oy 61 GAPSELHLQSQYRSNKTKQTVAAGRSWVAIPREQLTMSDKLLVMGTGKAGPLPPVPV 120

Db 61 GAPSELHLQSQYRSNKTKQTVAAGRSWVAIPREQLTMSDKLLVMGTGKAGPLPPVPV 120

Oy 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180

Db 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180

Oy 181 PELKTIPTIPVEIQDELEATGKYVGRCRMEKEEDLWGENSPILSFOTPPSPAKDVWVG 240

Db 181 PELKTIPTIPVEIQDELEATGKYVGRCRMEKEEDLWGENSPILSFOTPPSPAKDVWVG 240

Oy 241 NLCGTGPGGEEPLLKAPGPCVQVSKVFWVGGRELSPGEGITCCSLIPSGAEWARVA 300

Db 241 NLCGTGPGGEEPLLKAPGPCVQVSKVFWVGGRELSPGEGITCCSLIPSGAEWARVA 300

Oy 301 VNATSWEPLTNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPGPELHVVDWARDGD 360

Db 301 VNATSWEPLTNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPGPELHVVDWARDGD 360

Db 301 VNATSWEPLTNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPGPELHVVDWARDGD 360

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QY 361 PLEKLNVRLLPPGNLSALLPGNFTVGVYRITVTAVSASGLASSVWVGFPREELAPLVGP 420
|||||
Db 361 PLEKLNVRLLPPGNLSALLPGNFTVGVYRITVTAVSASGLASSVWVGFPREELAPLVGP 420
|||||
QY 421 TMLRLQDAPGCTPAIANGVPRHOLRGHLTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDL 480
|||||
Db 421 TMLRLQDAPGCTPAIANGVPRHOLRGHLTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDL 480
|||||
QY 481 PWGPELWVTAFTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
|||||
Db 481 PWGPELWVTAFTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLGCGLSLATSG 540
|||||
QY 541 RCYHLRHKVLPRWWEKVPDPANSSSGQPHMEQVPEAQPLGDLPLILEVEEMPPPPVWESS 600
|||||
Db 541 RCYHLRHKVLPRWWEKVPDPANSSSGQPHMEQVPEAQPLGDLPLILEVEEMPPPPVWESS 600
|||||
QY 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRQVLA 636
|||||
Db 601 QPAQATAPLDSGYEKHFLPTPEELGGLGPPRQVLA 636
|||||
RESULT 2
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
R:Accession: JH0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sod
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0329
A:Molecule type: mRNA
A:Residues: 1-783 <L>R>
A:Cross-references: GB:X55720; NID:g31698; PIDN:CAA39252.1; PID:g31699
A:Experimental source: placenta
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <M
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 8.5%; Score 298.5; DB 2; Length 783;
Local Similarity 22.5%; Pred. No. 9,7e-13;
hes 160; Conservative 75; Mismatches 250; Indels 227; Gaps 34;
QY 50 LNCWPEPLDGLGAPSELHLSQKYSR-N-KTQTVAV-----AAGRSWVAIPREOLTMDSKL 103
|||||
Db 140 LICOWEPGPETHLPTSTFLKSPKRCNCQTQGSILDCVPKQDSHCCIPRKHLLYQNM 199
|||||
QY 104 LVN-----GTAGQPLW-----PPVFNLETQKNAPRLG-----PDVDF 139
|||||
Db 200 GIWVQENALGTSNQLCLDPMVDVVKLEPPMLRTMDPSPEAPPAQGLQLCWEP----- 255
|||||
QY 140 SEDDPLEATVHMAPPTWPSHKVLICOF-HYRRCQEAATWILPELKTPIPTPVEIQDLLEL 198
|||||
Db 256 -----WQPGHLINQK-----CELRHKPQKGEASWALVG-----LPLEALQYEL 294
|||||
QY 199 -----ATGKYVYGRCRMEKEDLWGEWSPILSFQTPPSAPK-----DYVWSGNLCGTPGEE 250
|||||
Db 295 CGLLPATAVTLQIRCIWPLPGHWSNPSLSLELRTTERTAPTVELDTW----- 341
|||||
QY 257 LLLWKAQPCVQVSYKVFVWVGRELSPEGITCCCSLIPSGAEWAVRSVAVNATSNEP-- 308
|||||
Db 342 ---WRQ-----RQLDPRTVQLFWKVPVPLEDSGRIOGY-VVSWRPSG 379
|||||
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335
|||||
Db 380 QAGAILPLCNTELSTFHLPSAEQVALVAVNAGTSRPTVPVFSRSGPALTRUHAMA 439
|||||
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QY 336 ----ELLVTWQPGPGPBLEHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGV 388
|||||
Db 440 ROPHSLSWGWEPNPWPQGVYVIEWGLGPPSASNSKNTWRMEQNGRATGFLLENIRPFQL 499
|||||
QY 389 YRITVTAVSASGLASSVWVGFPREELAPLVGPTLWLRLQDAPGCTPAIANGVPRHOLRGH 448
|||||
Db 500 YEIVTPLYQDTMGPSORHYAYSQEMAPSHAPEL-HLKHGKHTWAQLEWVPEPELGKSP 558
|||||
QY 449 LTHYTLCAQSGTSPSCVMVSGNTQSVTLPLDPWGPCELW-----VTA 491
|||||
Db 559 LTHYTLFWTNAQNSQSAILNASSRGFVLHGLE--PASLYHHHLMAASAGATNSTVLT 616
|||||
QY 492 STRIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFL-----GCGLSLATSGRCYHLRHK 548
|||||
Db 617 MTLTPEGS-----ELHI-----ILGLFGLLLLTCLCG-----TAWLCCSPNRK 655
|||||
QY 549 VLPWRWWEKVPDPANSSSG-----QPHMEQVPEAQPLGDLPLILEVEEMPPPP-- 595
|||||
Db 656 ---NPLWPSVPDPAPSHSLGSLGWSVPTIMEADAFQLPGGLGTPPTTKLTVLDEEDKKVPWESH 712
|||||
QY 596 -----VMESSQPAQATAP-LDSGYEKHFLPTPEELGGLGPPR 631
|||||
Db 713 NSSETCGLPTLVQTYVVLQGDPRAVSTQPSQSG-----TSDQ---AGPPR 754
|||||
RESULT 3
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C>Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
R:Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <F>U>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A>Note: clones pHG11 and pHG5
A:Accession: A38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <F>U>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0330
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <F>U>
A:Cross-references: GB:X55721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A>Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A:Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 855-863 <S>E>T>
A:Cross-references: GB:S71484; NID:g240883; PIDN:AAB20660.1; PID:g240884
A:Experimental source: granulocyte
A>Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBI:P:71485)
R:Hanih, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:05:18 ; Search time 18.72 Seconds
(without alignments)
1245.664 Million cell updates/sec

Title: US-09-692-504-1

Perfect score: 3498

Sequence: 1 MRGRCAPFWLPLPKALL.....FLPTPEELGLGPPRPQVLA 636

Scoring_table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	380	10.9	862	1 I12S_HUMAN	Q99665 homo sapien
2	328.5	9.4	874	1 I12S_MOUSE	P97378 mus musculus
3	297.5	8.5	836	1 GCSR_HUMAN	Q99062 homo sapien
4	277	7.9	837	1 GCSR_MOUSE	P40223 mus musculus
5	250	7.1	918	1 I16B_HUMAN	P40189 homo sapien
6	248	7.1	917	1 I16B_MOUSE	Q00560 mus musculus
7	226.5	6.5	918	1 IL6B_RAT	P40190 rattus norv
8	206.5	5.9	1097	1 LIFR_HUMAN	P42702 homo sapien
9	206	5.9	1092	1 LIFR_MOUSE	P42703 mus musculus
10	169.5	4.8	1711	1 PTPO_RAT	Q64612 rattus norv
11	160.5	4.6	887	1 UFO_HUMAN	P30530 homo sapien
12	157.5	4.5	1705	1 PTPO_MOUSE	P70289 mus musculus
13	155.5	4.4	1270	1 MYPC_MOUSE	O70468 mus musculus
14	154.5	4.4	880	1 TVO3_MOUSE	P55144 mus musculus
15	154.5	4.4	3067	1 CALC_MOUSE	Q60847 mus musculus
16	151	4.3	1274	1 MYPC_HUMAN	Q14896 homo sapien
17	150	4.3	888	1 UFO_MOUSE	Q00993 mus musculus
18	147.5	4.2	1302	1 NRG_MOUSE	P20241 drosophila
19	146	4.2	4289	1 TENX_HUMAN	P22105 homo sapien
20	144	4.1	890	1 TVO3_HUMAN	Q06418 homo sapien
21	143.5	4.1	3063	1 CALC_HUMAN	Q99715 homo sapien
22	142	4.1	880	1 TVO3_RAT	P55146 rattus norv
23	138.5	4.0	581	1 PRLR_BOVIN	Q28172 bos taurus
24	137	3.9	1257	1 CAML_HUMAN	P32004 homo sapien
25	137	3.9	1284	1 NRCA_CHICK	P35331 gallus gall
26	136	3.9	2944	1 CAL17_HUMAN	Q02388 homo sapien
27	135	3.9	3164	1 TEGU_HSV1	P10220 herpes simp
28	134.5	3.8	1162	1 LEPR_RAT	Q62959 rattus norv
29	134.5	3.8	1912	1 PTPO_HUMAN	P23468 homo sapien
30	133.5	3.8	1142	1 MYPF_HUMAN	Q14324 homo sapien
31	133	3.8	1266	1 NGCA_CHICK	Q03696 gallus gall
32	133	3.8	1897	1 PTPE_HUMAN	P10586 homo sapien
33	132.5	3.8	1328	1 F1NC_PLEWA	Q91289 pleurodeles

ALIGNMENTS

RESULT 1
I12S_HUMAN

ID I12S_HUMAN STANDARD; PRT; 862 AA.

AC Q99665;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-

DE 2) (IL-12R-BETA2).

GN IL12RB2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97098510; PubMed=8943050;

RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,

RA Gately M.K., Gubler U.;

RT "A functional interleukin 12 receptor complex is composed of two

RT beta-type cytokine receptor subunits.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).

CC -!- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A

CC LOW AFFINITY.

CC -!- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH

CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND

CC IL12RB2.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC -----

CC EMBL; U64198; AAB36675.1; -

CC HSSP; P40189; LBQU.

CC MIN; 601642; -

CC InterPro; IPR002996; CRIA.

CC InterPro; IPR001777; FN.III.

CC InterPro; IPR003529; Hematopo_rcptor_L_F2.

CC Pfam; PF00041; fn3; 3.

CC SMART; SM00060; FN3; 3.

CC PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.

CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 21

FT CHAIN 22 862

FT DOMAIN 22 624

FT TRANSMEM 625 641

FT DOMAIN 642 862

FT DOMAIN 224 306

FT DOMAIN 421 508

FT DOMAIN 519 607 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 862 AA; 97134 MW; 67C0E0D946B8DD58 CRC64;

Query Match 10.9%; Score 380; DB 1; Length 862;
Best Local Similarity 25.3%; Pred. No. 3.2e-19;
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGSAGPLOCYGVGLDNLCSWEPLGD-----LGARSELHLQSQ----- 71
Db 126 QPON-----LSCIQKGEQGVACTWGERGTHLYTEVTLQSLGPKNLTWQCKDIYCDYL 181
QY 72 -----KYRSNKTQTV-AVAAGRSWAIPREQLTMSDKLLVWGTKAGQPLWPPVFN 121
Db 182 DFGINLTPESPENFTAKVTAVNSLSSSSSLP-STTFIDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNAPRLGPDVDFSEDDHLEATVHWAPPTWPSHKVLIQCFHYRRCQEAATLLEP 181
Db 232 IKFQ-KASVSR-----CTLYWR-----DEGLVLLNRLRYPSNSRLWN--- 269
QY 182 ELKTIPTLPV-----ETQDLELATGYKYVGRCRMEKEEDLWGESPILSFOTPP---PSAPK 234
Db 270 -----VNVTKAKGRHDLDLKPFTEYEQISSKHLHYKGSWSDSESURAGTPPEEPTGML 325
QY 235 DVWVSGNLCTPGGEEPELLLWK-----APGCVQVSYKVMFVWVGRELSP-----GITCCC 286
Db 326 DVWYMKRHIDY-SRQISLFWKNLVSSEARGKILHYQVTLQELTGKAMTQNTIGHTSWT 384
QY 287 SLIPSGAEWA-RVSAVNA-----TSHEPLTNLSVLCDLSASAPRSVAVSSIASTELLVTWQP 343
Db 385 TVIPRTGNWAVAVSAANSKSGSLPTRINIMNLCEAGLLAPROVSANS-EGMDNILVTWQP 443
QY 344 ---GPGEPLEHVVDWAR---DGPDELEKNVRLPPGNLSALLPGNFTVGVPPYRITVTAVS 397
Db 444 PRKDPNAVQEVYVWEVRELHPGDTQVPLNWRSRPTNVSALESNTKSYCYEIRVYALS 503
QY 398 ASGLASSVWGFREELAPLVGTLNRLQDAPGCPTRAIANGVPRHQLRGLHLYTIC-- 455
Db 504 GD-QGGCSSILGSKKAPLSGPHAINATE-EKGSILISNSIPVQEQMSCLLHYRIYWK 561
QY 456 -AUGSTPSVVC-----MNVSGNTQSVTLPLDLPWGPCELWVTASTAGQPPGPIRLHLHPDN 511
Db 562 ERDSNSQPLCEIPYRVSONSHPIINSIQ-PRVTYVLWMTALTAAAGESSHGNEREFCL-QG 619
QY 512 TLRWK--VLPGI---LFLWGLFLILGGLSLATSGRCYVHLRHKVL-----PRWVWEKVP 559
Db 620 KANWMAFVAPSIATIMVGIF-----STHIFQKVFVLLAALRPQWCSREIP 667
QY 560 DPANSSSQPH-----MEQVPEAQPLGDLPLILEVEEMPPVMESSQPAQATA-----PLD 610
Db 668 DPANSTCAKKYPIAEKTLPLDLRLDLDWTPTE-----DPEPLVISEVHLQVTPVFRHPPC 723
QY 611 SGYEKHELPTPEELGLLG-----PPRQOVL 635
Db 724 SNMPQ-----REKGIQGHQASHKMDMHSSAPPPPRAL 756

RESULT 2

112S_MOUSE
ID 112S_MOUSE STANDARD; PRT; 874 AA.
AC P97378;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-

DE 2) (IL-12R-BETA2).
GN IL12RB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; PubMed=8943050;
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RA Gately M.K., Gubler U.;
RT "A functional interleukin 12 receptor complex is composed of two
RT beta-type cytokine receptor subunits.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -!- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
CC LOW AFFINITY.
CC -!- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U64199; AAB36676.1; -;
DR HSSP; P40189; 1BQU.
DR MGD; MGI:1270861; IL12rb2.
DR InterPro; IPR002996; CRJA.
DR InterPro; IPR001777; FN.III.
DR InterPro; IPR003529; Hematopo_rcptor_L_F2.
DR Pfam; PF00411; fn3; 4.
DR PRINTS; PRO0014; PNTYPEIII.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
KW SIGNAL 1 20
FT CHAIN 1 874
FT INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.
FT DOMAIN 21 639
FT TRANSMEM 640 656
FT DOMAIN 657 874
FT DOMAIN 137 230
FT DOMAIN 240 322
FT DOMAIN 436 523
FT DOMAIN 534 622
FT CARBOHYD 48 48
FT CARBOHYD 101 101
FT CARBOHYD 114 114
FT CARBOHYD 142 142
FT CARBOHYD 151 151
FT CARBOHYD 169 169
FT CARBOHYD 179 179
FT CARBOHYD 224 224
FT CARBOHYD 252 252
FT CARBOHYD 279 279
FT CARBOHYD 287 287
FT CARBOHYD 323 323
FT CARBOHYD 391 391
FT CARBOHYD 495 495
SQ SEQUENCE 874 AA; 98196 MW; 582E4D21BF1FBD67 CRC64;

Query Match 9.4%; Score 328.5; DB 1; Length 874;
Best Local Similarity 23.0%; Pred. No. 1.3e-15;
Matches 153; Conservative 91; Mismatches 268; Indels 153; Gaps 32;

QY 39 LQCYGVGPIGLDNLCSWEP-----LGDIGAPSELHLQSKYRSNKTQ----- 79

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:04:33 ; Search time 50.89 Seconds
(without alignments)
1828.045 Million cell updates/sec

Title: US-09-692-504-1
Perfect score: 3498
Sequence: 1 MRGGRGAPFWLPLPKALL.....FLTPBELGLLGP RPQVLA 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3498	100.0	636	4 060624	O60624 homo sapien
2	2044	58.4	623	11 070394	Q70394 mus musculu
3	326.5	9.3	861	6 09BEG2	Q9beg2 bos taurus
4	292	8.3	971	11 070458	Q70458 mus musculu
5	288.5	8.2	970	11 088821	O88821 mus musculu
6	241.5	6.9	918	13 09W609	Q9w609 gallus gall
7	237.5	6.8	881	13 057519	O57519 xenopus lae
8	229	6.5	710	13 057520	O57520 xenopus lae
9	226	6.5	979	4 096650	Q96650 homo sapien
10	212	6.1	1093	11 070535	O70535 rattus norv
11	191	5.5	1236	4 09UH13	Q9uh13 homo sapien
12	191	5.5	1308	4 09UH14	Q9uh14 homo sapien
13	187.5	5.4	1180	4 015051	O15051 homo sapien
14	180.5	5.2	1299	4 015179	O15179 homo sapien
15	180	5.1	1299	4 032823	Q92823 homo sapien
16	173.5	5.0	1264	5 091767	P91767 manduca sex
17	168	4.8	1154	11 09QVN3	Q9qvn3 rattus sp.
18	166.5	4.8	1146	13 0918V6	Q9i8v6 gallus gall
19	166.5	4.8	1166	11 09QVN4	Q9qvn4 rattus sp.

20	166.5	4.8	1215	11	P97686	P97686 rattus norv
21	164.5	4.7	1185	4	Q9NTD2	Q9ntd2 homo sapien
22	163.5	4.7	1705	11	O9ERK5	O9erk5 mus musculu
23	162.5	4.6	1197	13	Q90478	Q90478 brachydanio
24	161.5	4.6	1598	4	Q9P214	Q9p214 homo sapien
25	160	4.6	1148	13	Q9IBA7	Q9iba7 gallus gall
26	159.5	4.6	4280	5	Q9UB29	Q9ub29 caenorhabdi
27	159.5	4.6	4450	5	Q9UB28	Q9ub28 caenorhabdi
28	156	4.5	1274	4	Q9UM53	Q9um53 homo sapien
29	155.5	4.4	1147	13	Q9DDK1	Q9ddk1 meleagris g
30	151.5	4.3	2944	11	O63870	O63870 mus musculu
31	151	4.3	1914	13	Q91008	Q91008 gallus gall
32	150	4.3	890	11	Q9Z1A0	Q9z1a0 cavia porce
33	150	4.3	1232	13	Q90284	Q90284 carassius a
34	147.5	4.2	800	11	O63257	O63257 rattus norv
35	147	4.2	1948	4	Q13332	Q13332 homo sapien
36	146	4.2	876	11	O60752	O60752 mus musculu
37	146	4.2	1894	11	O64487	O64487 mus musculu
38	146	4.2	4288	4	Q9NPK9	Q9npk9 homo sapien
39	145.5	4.2	476	11	O9CU34	O9cu34 mus musculu
40	144	4.1	884	4	O14953	O14953 homo sapien
41	144	4.1	1399	4	O75870	O75870 homo sapien
42	143.5	4.1	4135	6	O18977	O18977 bos taurus
43	142.5	4.1	1898	11	O64604	O64604 r protein-t
44	141.5	4.0	1904	11	O64699	O64699 mus musculu
45	140.5	4.0	801	11	Q9WTM8	Q9wtm8 rattus norv

ALIGNMENTS

RESULT 1					
O60624					
ID	O60624	PRELIMINARY;	PRT;	636 AA.	
AC	O60624;				
DT	01-AUG-1998 (Tremblrel. 07, Created)				
DT	01-AUG-1998 (Tremblrel. 07, Last sequence update)				
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)				
DE	CLASS I CYTOKINE RECEPTOR (CRL1 PROTEIN).				
GN	WSX1 OR CRL1				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98262921; PubMed=9600072;				
RA	Sprecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,				
RA	Schrader S.K., Yamagiwa T., Whitmore T.E., O'Hara P.J., Foster D.F.;				
RT	"Cloning and characterization of a novel class I cytokine receptor.";				
RL	Biochem. Biophys. Res. Commun. 246:82-90(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Zhang W., Wan T., He L., Yuan Z., Cao X.;				
RT	"A novel gp130-like cytokine receptor.";				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF053004; AAC39755.1;				
DR	EMBL; AF106912; AAC36090.1;				
DR	InterPro; IPR003961; FN_III.				
DR	Pfam; PF00041; fn3; 2.				
DR	SMART; SM00060; FN3; 1.				
SQ	SEQUENCE 636 AA; 69473 MW; DC7DAAABA643CE97 CRC64;				
Query Match 100.0%; Score 3498; DB 4; Length 636;					
Best Local Similarity 100.0%; Pred. No. 4.3e-251;					
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MRGGRGAPFWLPLPKALLPLLVLFQTRPQGSAGPLQCYGVGPLDNC	SWEPLGDL	60	
Db	1	MRGGRGAPFWLPLPKALLPLLVLFQTRPQGSAGPLQCYGVGPLDNC	SWEPLGDL	60	
Qy	61	GAPSELHQSQYRSNKTQTVAAGRSWVAIPREQLTMSDKLLVMGT	KAGQPLPPV	120	

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Db 61 GAPSEHLQSKYRSNKTQTVAAAGRSWAIPREQLTMSDKLLVWGTAKAGQPLWPPVFV 120
QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQPHYRRCOEAAWTLLE 180
Db 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQPHYRRCOEAAWTLLE 180
QY 181 PELKTIPLTPVEIQDLELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVWSG 240
Db 181 PELKTIPLTPVEIQDLELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVWSG 240
QY 241 NLCGTGGGEEPLLWKAPGPCVQVSYKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300
Db 241 NLCGTGGGEEPLLWKAPGPCVQVSYKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300
QY 301 VNATSWEPITNLVCLDSASAPRSVAVSSVAGSTELLTWQPGCEPLEHVVDWARDGD 360
Db 301 VNATSWEPITNLVCLDSASAPRSVAVSSVAGSTELLTWQPGCEPLEHVVDWARDGD 360
QY 361 PLEKLNWRLLPGLNLSALLPGNFTVGVYRITVTAVSASGLASASSVMWGFREELAPLVGP 420
Db 361 PLEKLNWRLLPGLNLSALLPGNFTVGVYRITVTAVSASGLASASSVMWGFREELAPLVGP 420
QY 421 TLWRLQDAPPGTAPAIWGEVPRHQLRGHLTHYTLCAQSGTSPVCMVNSGNTQSVTLPLD 480
Db 421 TLWRLQDAPPGTAPAIWGEVPRHQLRGHLTHYTLCAQSGTSPVCMVNSGNTQSVTLPLD 480
QY 481 PWGPCELWLTASTIAGQGGPPIRLRHLPDNTLRWKVLPGLFLWGLFLGCGLSLATS 540
Db 481 PWGPCELWLTASTIAGQGGPPIRLRHLPDNTLRWKVLPGLFLWGLFLGCGLSLATS 540
QY 541 RCYHLRHKVLPWRWKEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVWESS 600
Db 541 RCYHLRHKVLPWRWKEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVWESS 600
QY 601 QPAQATAPLDGSEYKHFLLTPPELGLLGGPPRQVLA 636
Db 601 QPAQATAPLDGSEYKHFLLTPPELGLLGGPPRQVLA 636
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RESULT 2
O70394 PRELIMINARY; PRT; 623 AA.
AC O70394;
DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
DE 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GS WSX1.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98262921; PubMed=9600072;
RA Schreder C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,
RA Schreder S.K., Yamagata T., Whitmore T.E., O'Hara P.J., Foster D.F.;
RT "Cloning and characterization of a novel class I cytokine receptor.";
RL Biochem. Biophys. Res. Commun. 246:82-90(1998).
DR EMBL; AF053005; AAC40121.1; -.
DR MGD; MGI:1355318; WSX1.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 623 AA; 68998 MW; 4BA20FEC875A7180 CRC64;
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Query Match 58.4%; Score 2044; DB 11; Length 623;
Best Local Similarity 62.8%; Pred. No. 2.2e-143;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;
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QY 14 LPKLAILLPLLVLFQTRPGSAGPLQCYGVGVLGDLNCSWEPGLDGLAPSELHLSQKY 73

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Db 9 LTPLELLLSLMSILLGTRPHSGPGLQCYSVGPLGLNCSWEPGLDLETPPVLYHQSQKY 68
QY 74 RSNKTQTVAAAGRSWAIPREQLTMSDKLLVWGTAKAGQPLWPPVFVNLETKMKNAPRL 133
Db 69 HENRWEVAVKSPKQSWVTIPREQFTNADKLLIWGTOKGRPLMSSVSNLETKMKNAPRL 128
QY 134 GPDVDFSEDDPLEATVHWAPPTWPSHKVLICQPHYRRCOEAAWTLLEPELKIPLTPVEI 193
Db 129 FSQVDISEEATLEATVQWAPPVPPQKALTQCFRYKECAEAWTRLEPQLKTGLTPVEM 188
QY 194 ODLELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVNSGNCGTGGGEEPLL 253
Db 189 QNLEPGTCYQVGRGCVENGYP-WGEWSSPLSFQTPFLDPEDVWVSGTVCETSGKRAALL 247
QY 254 LNKAPGPCVQVSYKVMFWVGGRELSPEGITCCCSLIPSGAEWARVSAVNATSWEPITNLS 313
Db 248 VKMDPRCPQVYTYVWFGAGDITTCQEEVPCCKSPVPANMEWAVVSPGNSTSVPTNLS 307
QY 314 LVCLDSASAPRSVAVSSVAGSTELLTWQPGCEPLEHVVDWARDGDPLEKLNWRLLPGL 373
Db 308 LVCLAPESAPCDVGSADSGPGIKVTRKQGRKPLEYVVDWAQDGLSKLNWTRLLPG 367
QY 374 NLSALLPGNFTVGVYRITVTAVSASGLASASSVMWGFREELAPLVGTLWRLQDAPPGT 433
Db 368 NLSTLLPGEFKGVYRITVTAVYSGGLAAPSVWGFREELVPLAGAVWRLPDDPPGTP 427
QY 434 ATAWGVPVRHQLRGHLTHYTLCAQSGTSPVCMVNSGNTQSVTLPLDLPWGPCELWLTAST 493
Db 428 VVWAGVPRHQLRGQATHYTCIQSRGLSTVCRNVSSQTQATLPLNHSGSFKLWTVST 487
QY 494 IAGQGGPPIRLRHLPDNTLRWKVLPGLFLWGLFLGCGLSLATS----GRCYHLRHKV 549
Db 488 VAGQGGPGLSHLDPNIRKALPWFSLWGLLWGLLWGLLWGLSLASTRCQARCLHWRHKL 547
QY 550 LPRWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPVWESSQPAQATAPL 609
Db 548 LPQWIWVRVDPDPANSSGQPHYKEVSLPQPPKDGPILEVEEVELQPVVSES---PKASAPI 604
QY 610 DSGYEKHFLLTPPELGLL 627
Db 605 YSGYEKHFLLTPPELGLL 622
```

```
RESULT 3
Q9BEG2 PRELIMINARY; PRT; 861 AA.
AC Q9BEG2;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE IL-12 RECEPTOR BETA2 PRECURSOR.
GN IL-12R BETA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH NODE;
RA Waldvogel A.S., Zakher A., Heussler V.T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ308426; CAC28320.1; -.
KW Signal; Receptor.
FT SIGNAL 1 23 POTENTIAL
FT CHAIN 24 861 IL-12 RECEPTOR BETA2
SQ SEQUENCE 861 AA; 96208 MW; 4B7B1ESD1E358E5B CRC64;
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```
Query Match 9.3%; Score 326.5; DB 6; Length 861;
Best Local Similarity 24.5%; Pred. No. 5.3e-16;
Matches 171; Conservative 88; Mismatches 281; Indels 157; Gaps 36;
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QY 39 LQCYGVPLGDLNCSWEPLGD-----LGAPSELHLQSQ----- 71
Db 130 LSCIQKGERGTCTWHRGRDTHLYTAYTLQNLGPKNTWQKQNDHYCDHLDLGINLTP 189
QY 72 -KYRSNKT-OTVAVAGRSWAIPREQLTMSDKLLVWGTGKAGPLPPVFNLETOMKPN 129
Db 190 BSLESSYTKVTAINSLGASFP-FSFTLLDIV-----RPL-PPWDRIKF----- 234
QY 130 APRLGPVDSEDDPLEATVHWAPPTWPSHKVLICQHYRCQEAATLLEPELKTIPLT 189
Db 235 -----VNASVDO-----RCTLWR-----DEGLVLLNRLRYRPNRSNWNVN---VTNKG 277
QY 190 PVEIQDLATGYKYVGRCKEKEEDLNGEWSPLSFOTPPSAP-----KDVW-----VSGN 241
Db 278 RHDLLDKPFTFEYEQISSKHLHYKGSMSDSLSRTQTPPEEPIGMLNVWYMRQHIDYN 337
QY 242 LCGTPGGEPELHMK-----APGCVQVSYKVFVW-VGGRLESPGTTCCS-----LIPS 291
Db 338 -----ROOISLFWKLNLSLSEARGKILH--YQVTLQKYGAGEITLQNTTEHTSWTWIPIR 389
QY 292 GAEW-ARVSAYNA--TSWEPTNLISLVLDLSASAPRSVAVSSIAGSTELLVTWOP---GP 345
Db 390 TGNMAAASVANSKSSLPTRINITDLCGAELLAQOVLAKS-EGMDKLWWTWTPPEKAT 448
QY 346 GEPLHVVWVARDGP-----LEKLNWRLPGLNLSALLPGNFTVGPYRITVTAVSASGL 401
Db 449 AAVQEVVWV-RELHPGAGMPPGLWLSPPYRLSALISENIKPYICVEIRVHAL-AGDQ 506
QY 402 ASASVNGFREELAPLVGPTLWRLQDAPPTATANGVPRHQLRGLHTHYTLG-----AQS 458
Db 507 GGCSTRNSQHKAPLSPHNAISE-EKGSVLISWDEIPAREQMGCLHYRIYWKERDS 565
QY 459 GTSPSVC---MNVSGNTQSVTLPLDLPWPCELWMTASTIAGQPPGPTLRLHLPDNTLRW 515
Db 566 NSQPOLCEIPYRISNHPIDSLQ-PRVYVLMWLTALTAAGESQGNRECL-QGKANW 623
QY 516 KVLPGILFLWGLFLGGLSLATSGRCYHLRHKL-----PRWVWEKVPDPANSSSQPH 570
Db 624 STFVAPSTCMAMVWG-----VLSMRFRQKVFVLLALRPQWCKEIPDPANSTWAKKY 678
QY 571 MEQVPEAQPLGDLPLE-----VEEMEP-----PP-----VMSSQPAQA--T 606
Db 679 PIVEKTLQALDRLLTWTPEPEPEPLVINEVLCRVTPVFRPHHRSWSEKGGVQGHYT 738
QY 607 APLDSGYEKHFLTP-----BELGLIGP 629
Db 739 SEEDTGYSASSPPPPRAPTAETGQGVLDLYKVLGSKGP 775
RESULT 4
ID 070458 PRELIMINARY; PRT; 971 AA.
AC 070458:
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ONCOSTATIN M SPECIFIC RECEPTOR.
GN OSMR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98252923; PubMed=9584176;
RA Lindberg R.A., Juan T., Welcher A.A., Sun Y., Cupples R., Guthrie B.,
RA Fletcher F.A.;
RT "Cloning and characterization of a specific receptor for mouse
RT oncostatin M."
RL Mol. Cell. Biol. 18:3357-3367(1998).
DR ENBL; AF058805; AAC40122.1; -;
DR HSSP; P40189; 1BQU.

DR MGI:1330819; Osmr.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
SQ SEQUENCE 971 AA; 110229 MW; BECAA85BBD47C1E7 CRC64;
Query Match 8.3%; Score 292; DB 11; Length 971;
Best Local Similarity 22.9%; Pred. No. 2.2e-13;
Matches 159; Conservative 87; Mismatches 275; Indels 174; Gaps 34;
QY 50 LNCWEPLGDLGAPSELHLQSQYR-----SNKTQTVAVAGRSWAIPREQ----- 96
Db 250 LDCSEPE---GVDTTLRKQRFQNYTLCSFSKCEVSNTRNSYTWQITGSGEMYNF 305
QY 97 -LTMSSDKLLVWGTGKAGPLPPVFNLETOMKPNAPRLGPDVDFSEDDPLEATVHWAPPT 155
Db 306 TLTAENQLRKRSVN-----INFNLTRVHPKAPQ---DVTLKIATKANWTWKVHS 354
QY 156 WPSKVLICQHYRCQEAATLLEPELKTIPLTVEIQDLATGYKYVGRCKEKEED 215
Db 355 HGNNYTLCCQVKLOYGE---VIHEHNSVHMSANYLFSLDLDPDTKYKAFVRCASANHFW 410
QY 216 LWGEWSPLSFOTPPSAPK---DVMVSGNLCTGCGEPEPLLLKAPGCVQ-----VS 265
Db 411 KWSMDTQ-KEFTPTAPSAQALDWM--RQVWSENGRRIVTLFWK---PLLKSQANGKIIIS 464
QY 266 YKMFVWVGRELSPGITCCGSLIPSGAWEA-----VWAPALSTNLSDLDQPKIRITNNSGASP- 513
Db 465 YNI---VVENEAKPTSEHYC-----VWAPALSTNLSDLDQPKIRITNNSGASP- 513
QY 310 TNLISVLCLDSASAPRSVAVSSIAGSTELL-VTWQPGCEPLEHVVDM-ARQGDPLEKLNW 367
Db 514 ---ESLWVLSNDSGHBEVEKTEKIGKDAFNISWEVSGDTMGVYVVDWCAHSQDQCDLQW 571
QY 368 VRLPPGNLSALLPG-NFTVGPYRITVTAVSASGLAS-ASSVWGFREELAPLVGPTLWRL 425
Db 572 KNLGNTTSTITSDDFKPGVYRIFERSVEHKAIRLVEKQRTQELAPLVNPKV--- 628
QY 426 QDAPPGTP---AIANGVEPRHQLRGLHLYTLCAQS-----GTSPSVCNM 467
Db 629 -EIPYSTNSFVLRWPDYDSDFQAGFKGLVYVVKSEKQWQWERTLLPDNSVLCKYD 687
QY 468 VSGN-TQSVTLPLDLP-WGCPCELWMTASTIAGQPPGPTLRLHLPDNTLRWVLPGLFLW 525
Db 688 INGSETKTLTVENLQPELSLEYEFFVTPTYSAGPGPNETFTKVTTPD--ARSHMLLIQILPM 745
QY 526 GLFLIGLGLSLATSGRCYHLRHKLPRWWEK---VDPANSS----- 565
Db 746 TLCVL---LSIIV---CYW-----KQWVKEKCYPDIPNPKSSILSLIKSKKNPHLLMN 794
QY 566 -----SGQPHMEQVPEAQPLGDLPLEVEEMEPVPPVMESSQ 601
Db 795 VKDCIPDVLEVINKAEGSKTCVSGKGLHIEDVPTKPI--VP-TEKDSSGVPVPCIFPEN 851
QY 602 PAQATAPLDSGYEKHFL-----TPPELGLLIGPP 630
Db 852 FTYDOSAFDSG--SHGLIPGLPKDTAHLQLGLLAPP 884
RESULT 5
O88821 PRELIMINARY; PRT; 970 AA.
ID O88821
AC O88821;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ONCOSTATIN M RECEPTOR BETA.
GN OSMR.
OS Mus musculus (Mouse).

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:03:48 ; Search time 43.01 Seconds
(without alignments)
1095.341 Million cell updates/sec

Title: US-09-692-504-1

Perfect score: 3498

Sequence: 1 MRGGRGAPFWLPLPKALL.....FLTPPEELGLGPPRPQVLA 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
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 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	636	19 AAW33399	Alternatively spli
2	3498	100.0	636	22 AAU01853	Human type I cyto
3	3490	99.8	636	20 AAY29781	Human DNAX cyto
4	3150	90.1	578	19 AAW33398	Human haematopoiet
5	2875	82.2	523	20 AAY29785	Partial human DNAX
6	2044	58.4	623	19 AAW33400	Mouse haematopoiet
7	2044	58.4	623	22 AAU01854	Mouse type I cyto
8	886.5	25.3	246	20 AAY29786	Partial mouse DNAX
9	400	11.4	150	20 AAY29782	Mouse DNAX cyto
10	380	10.9	862	18 AAW12771	Human interleukin-
11	298.5	8.5	783	12 AAR11741	Granulocyte colony

12	298.5	8.5	783	16	AAW77868	Human placental G-
13	298.5	8.5	783	18	AAW10485	Human granulocyte
14	297.5	8.5	800	18	AAW10486	Human granulocyte
15	297.5	8.5	801	12	AAR11742	Clone 25-1 encoded
16	297.5	8.5	813	21	AAB03873	Human granulocyte
17	297.5	8.5	836	12	AAR14255	Human GCSF recepto
18	293	8.4	873	22	AAU02905	Angiotensin conver
19	292	8.3	863	12	AAR14257	Human GCSF recepto
20	275	7.9	837	12	AAR14254	Murine GCSF recept
21	268.5	7.7	771	12	AAR14256	Human GCSF recepto
22	268.5	7.7	824	22	AAM23678	Human EST encoded
23	251	7.2	917	13	AAR26334	gpi30. Mus muscul
24	250	7.1	918	15	AAR46233	Human soluble gly
25	250	7.1	918	21	AAY44694	Human gpi30 protei
26	249	7.1	775	22	AAU02904	Angiotensin conver
27	249	7.1	918	12	AAR10545	Recombinant human
28	248	7.1	708	17	AAR85911	gpi30 N-terminal f
29	248	7.1	917	21	AAY55073	Mouse gpi30 protei
30	247	7.1	918	17	AAR53568	Human gpi30 protei
31	235	6.7	708	14	AAR37804	Human gpi30 N-term
32	231.5	6.6	603	21	AAY32222	Granulocyte colony
33	226	6.5	979	17	AAR85912	Oncostatin M recep
34	218.5	6.2	961	21	AAY92187	Human gpi30-J-C-ga
35	217.5	6.2	951	20	AAW70798	Human gpi30-C-gamm
36	217.5	6.2	951	21	AAY92186	Human gpi30-C-gamm
37	210	6.0	658	17	AAR94576	Human gpi30 splice
38	207	5.9	662	22	AAB51244	Human haemopoietin
39	206.5	5.9	1097	15	AAR49508	Human LIF-R. Homo
40	206.5	5.9	1097	15	AAR45776	Human leukaemia in
41	206.5	5.9	1097	16	AAR74097	Human leukaemia in
42	205	5.9	1001	15	AAR45774	Human leukaemia in
43	204	5.8	652	22	AAB51242	Human haemopoietin
44	204	5.8	727	21	AAY92192	Human gpi30-kappa
45	204	5.8	738	21	AAY92194	Human gpi30-J-kapp

ALIGNMENTS

RESULT 1
 AAW33399
 ID AAW33399 standard; Protein; 636 AA.
 AC AAW33399;
 DT 22-MAY-1998 (first entry)
 DE Alternatively spliced zcytor1.
 KW Human; haematopoietic cytokine receptor; Zcytor1; ligand detection;
 KW cancer diagnosis; agonist; antagonist; alternatively spliced.
 OS Homo sapiens.
 PN WO9744455-A1.
 PD 27-NOV-1997.
 PF 19-MAY-1997; 97WO-US08502.
 PR 23-MAY-1996; 96US-0653740.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
 DR WPI; 1998-018509/02.
 DR N-PSDB; AAT94120.
 PT Haematopoietic cytokine receptor - useful for ligand detection, and
 PT pathological condition diagnosis
 PS Claim 7; Pages 46-51; 86pp; English.

The present sequence is an alternatively spliced human
 haematopoietic cytokine receptor 2cytor1, useful for ligand
 detection, and pathological condition diagnosis, including cancer.
 Receptor agonists of the protein can be used to stimulate the
 proliferation and development of target cells in vitro and in vivo.
 The agonists can stimulate cell mediated immunity and lymphocyte
 proliferation, to treat infection involving immunosuppression, e.g.
 viral infections. They may also be used to suppress tumours, induce
 cytotoxicity, treat leukopenias and enhance the regeneration of
 the T-cell repertoire after bone marrow transplantation.
 Antagonists of the protein may be used to suppress the immune
 system, treat autoimmune diseases, including rheumatoid arthritis,
 multiple sclerosis and diabetes mellitus. Immune suppression caused
 by the antagonists can also be used to reduce rejection of tissue
 or organ transplants and grafts, and to treat T-cell specific
 leukaemias and lymphomas.

Query Match 100.0%; Score 3498; DB 19; Length 636;
 Best Local Similarity 100.0%; Pred. No. 2e-265;
 Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGGGAPFWLPLPKLALLPLLWLFQRTFQGSAGPLQCYGVGPLGDLNCSWEPLGDL 60
 DB 1 mrgggagpflwplpkallplllwlfqtrfpggsagplqcygvvgplgdlncswepldgl 60
 QY 61 GAPSELHLSQKYSRKNKTOTVAAGRSNVAIPREOLTHSDKLLVWGTAKGQPLWPPV 120
 DB 61 gapsehlhsqkysrskntotvaagrsnvaipreqlthmsdkllvwtgkagqplwppv 120
 QY 121 NLETKMPNAPRLGPDVDFSEDPLATVHWAPPTWPSHKVLICQPHYRRCOEAAWTLLE 180
 DB 121 nletkmknarplgpdvdfsedplvatwvappptwpskhvlicqphyrccoeaawtlle 180
 QY 181 PELKTIPLTPVEIQDLELATGYKVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
 DB 181 pelktipltvpeiqlatgykvgrcrmekeedlwgewspilsfqtppsapkdvwvsg 240
 QY 241 NLGCTPGGEPILLKAPGCVQVSKVFWVGGRELSPEGITCCCSLIPSGAEWARVSA 300
 DB 241 nlcgtpggpepilkapgcqvskvfwvggrelspegitcccslipsgaewarvsa 300
 QY 301 VNATSEPLTNLSVCLDSASAPRSVAVSISAGSTELLVTWQPGEPLEHVVDWARDGD 360
 DB 301 vnatspepltnlsvcldsasaprsavavsiasgstellvtwpggeplehvvwardgd 360
 QY 361 PLEKLNWRPLPGENLSALLPGNFTVGVPIYITVAVSASGLASASVWGFRLEAPLVGP 420
 DB 361 pleklnwvrlppgnlsallpgnftvgvpyitvtavsasglasasvvgfreelaplvgp 420
 QY 421 TLWRLODAPGTPAIANGVPRHQLRGHLTHYTLCAOSTSPSCVMNVSQNTQSVTLPLD 480
 DB 421 tlwrlodapgtpaiangvprhqlrghlthyltcaostspscvmnvsqntqsvtlpld 480
 QY 481 PMGPCBLWLTASTIAGQGGPGLRLHLPDNTRLRWKVLPGILFLWGLFLGCGLSLATSG 540
 DB 481 pmgpcblwltastiaqggpplrlhlpdntrlrwkvlpgilflwglflgclslatsg 540
 QY 541 RYVHLRHKVLPKRWWEKVPDPANSSGGQPHMEQVPAQPLGDLPLEVEEMEPPIPVWESS 600
 DB 541 rylvhlrhkvlprwwekvpdpanssgqphmeqvpaqplgdlpleveemepppvwess 600
 QY 601 QPAQATAPLDSGVEKHFTPEPLGLGPPRQVLA 636
 DB 601 qpaqatapidsgvekhftpeplglgpprpqvla 636

RESULT 2
 AAU01853
 ID AAU01853 standard; Protein: 636 AA.

XX AC AAU01853;
 XX DT 07-SEP-2001 (first entry)
 XX DE Human type I cytokine receptor, hTCCR.
 XX KW Human; type-I cytokine receptor; TCCR; T-cell differentiation;
 KW Th1; Th2; agonist; antagonist; autoimmune inflammatory disease;
 KW allograft rejection; multiple sclerosis; inflammatory bowel disease;
 KW insulin-dependent diabetes mellitus; infectious disease;
 KW human immunodeficiency virus; allergic disorder; asthma;
 KW allergic rhinitis; HIV.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..32
 FT Protein 33..636
 FT Region 41..54 Mature_hTCCR
 FT Modified-site 51..54 "Cytokine receptor family signature 1"
 FT Modified-site 76..79 "Asn is N-glycosylated"
 FT Modified-site 107..112 "Asn is N-glycosylated"
 FT Region 183..191
 FT Modified-site 240..245 "Region of homology with the second subunit
 FT Modified-site 244..249 of human granulocyte-macrophage colony-stimulating
 FT Modified-site 281..286 factor"
 FT Modified-site 292..297 /label= N_myristoylation_site
 FT Modified-site 302..305 /label= N_myristoylation_site
 FT Modified-site 311..314 /note= "Asn is N-glycosylated"
 FT Modified-site 373..378 /note= "Asn is N-glycosylated"
 FT Modified-site 374..377 /label= N_myristoylation_site
 FT Modified-site 382..385 /note= "Asn is N-glycosylated"
 FT Modified-site 400..405 /note= "Asn is N-glycosylated"
 FT Modified-site 459..464 /label= N_myristoylation_site
 FT Modified-site 467..470 /label= N_myristoylation_site
 FT Modified-site 470..475 /note= "Asn is N-glycosylated"
 FT Domain 517..538 /label= N_myristoylation_site
 FT Modified-site 522..532 /label= Transmembrane_domain
 FT Modified-site 531..536 /note= "Prokaryotic membrane lipid attachment site"
 FT Modified-site 533..538 /label= N_myristoylation_site
 FT Modified-site 563..566 /label= N_myristoylation_site
 FT Modified-site 563..566 /note= "Asn is N-glycosylated"
 XX WO200129070-A2.
 XX PD 26-APR-2001.

CC represents the specifically claimed human DCRS1, for use in the
composition of the present invention.

XX Sequence 636 AA;

Query Match 99.8%; Score 3490; DB 20; Length 636;
Best Local Similarity 99.7%; Pred. No. 8.3e-265;
Matches 634; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRGGGAPFWLWPKLALLPLLLWLFQRTPOGSGAPLQCYGVGGLDNCSEWPLGDL 60
Db 1 mrgggagpflwplkallplllwlfqtrpqgsagplqcygvglncswewplgdl 60
QY 61 GAPSELHLQSQKYSRNTQTVAAGRSWVAIPREOLTMDSKLLVWGTKAGOPLPVPFV 120
Db 61 gapsehlqsqkyrsnktqtvaagrswwaipreqtmsdkllvwgkagoplpvpfv 120
QY 121 NLEQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQEAATLLE 180
Db 121 nletqmkpnarlgpdrvdfseddpleatvhwappptwpskhvllcqfhyrcqeaawtlle 180
QY 181 PELKTIPLTPVETQDLELATGYKVGRCRMEKEEDLWGSWSPILSFQTTPSPAPKDVWVSG 240
Db 181 pelktipltpvetqdlelatgykvgrcrmekeedlwgspsilsfqtppsapkdvwvs 240
QY 241 NLCGTPGGEPLLLWKAPGCPQVQSVYKVFVWVGGRLESPGEGITCCSLIPSGAEWARVSA 300
Db 241 nlcgtpggeplllwkapgcpvqvsvykvfvwvvggrelspggitccslipsgaewarvsa 300
QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVAGSTELLVWPGPGEPLHVVVDWARDGD 360
Db 301 vnatswepitnlsvlcldsasaprsavassvagsstellvwpgpgeplehvvmdwardgd 360
QY 361 PLEKLNWVRLPGNLSALLPGNFTVGPVYRITVAVSAGLASASSVWGFREELAPLVGP 420
Db 361 pleklnwvrlpgnlsallpgnftvgpvyrityavssaglasassvwgfrelaplvgp 420
QY 421 TLWRQLDAPPGTPTAIWGEVPRHQLRGHLYTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLD 480
Db 421 tlwrqldappgtptaiwgevprrhqlrghlythyltcaqsgtspscvmnvsgntqsvtlpdl 480
QY 481 PNGPCBELWNTASTIAGQGGPPGPIRLHLPDNTLRWKLPGILFLWGLFLGCGLSLATSG 540
Db 481 pngpcbelwntastiaqggppgpiirlhlpdntlrwklpgilflwglflgclslatgs 540
QY 541 RCYHLRHKVLPRWWEKVPDPANSSSQPHMEQVPEAQPLGDLPILEVEEMEPVPMESS 600
Db 541 rcyhlrhkvlprwwekvpdpanssqphmeqvpeaqplgdlpileveemepvpmess 600
QY 601 QPAQATAPLDGSGYERHFLTPETPLGLGPPRPQVLA 636
Db 601 qpaqatapldsgyerhfltpetplglgpprpqvla 636

RESULT 4

AAW33398

XX ID AAW33398 standard; Protein; 578 AA.

XX AC AAW33398;

XX XX

XX 22-MAY-1998 (first entry)

XX Human haematopoietic cytokine receptor zcytor1.

XX Human; haematopoietic cytokine receptor; zcytor1; ligand detection;
XX Cancer diagnosis; agonist; antagonist.

XX Homo sapiens.

XX OS WO9744455-A1.

XX PN 27-NOV-1997.

XX PD

XX 19-MAY-1997; 97WO-US08502.

XX 23-MAY-1996; 96US-0653740.

XX (ZYMO) ZYMOGENETICS INC.

XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;

XX WPI: 1998-018509/02.

XX N-PSDB; AAT94119.

XX Haematopoietic cytokine receptor - useful for ligand detection, and
XX pathological condition diagnosis

XX Claim 1; Pages 39-43; 86pp; English.

XX The present sequence is the human haematopoietic cytokine
XX receptor zcytor1, useful for ligand detection, and pathological
XX condition diagnosis, including cancer. Receptor agonists of the
XX protein can be used to stimulate the proliferation and development
XX of target cells in vitro and in vivo. The agonists can stimulate
XX cell mediated immunity and lymphocyte proliferation, to treat
XX infection involving immunosuppression, e.g. viral infections. They
XX may also be used to suppress tumours, induce cytotoxicity, treat
XX leukopaenias and enhance the regeneration of the T-cell repertoire
XX after bone marrow transplantation. Antagonists of the protein may
XX be used to suppress the immune system, treat autoimmune diseases,
XX including rheumatoid arthritis, multiple sclerosis and diabetes
XX mellitus. Immune suppression caused by the antagonists can also be
XX used to reduce rejection of tissue or organ transplants and grafts,
XX and to treat T-cell specific leukaemias and lymphomas.

XX Sequence 578 AA;

Query Match 90.1%; Score 3150; DB 19; Length 578;

Best Local Similarity 90.9%; Pred. No. 3e-238;

Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

QY 1 MRGGGAPFWLWPKLALLPLLLWLFQRTPOGSGAPLQCYGVGGLDNCSEWPLGDL 60
Db 1 mrgggagpflwplkallplllwlfqtrpqgsagplqcygvglncswewplgdl 60
QY 61 GAPSELHLQSQKYSRNTQTVAAGRSWVAIPREOLTMDSKLLVWGTKAGOPLPVPFV 120
Db 61 gapsehlqsqkyrsnktqtvaagrswwaipreqtmsdkllvwgkagoplpvpfv 120
QY 121 NLEQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQEAATLLE 180
Db 121 nletqmkpnarlgpdrvdfseddpleatvhwappptwpskhvllcqfhyrcqeaawtlle 180
QY 181 PELKTIPLTPVETQDLELATGYKVGRCRMEKEEDLWGSWSPILSFQTTPSPAPKDVWVSG 240
Db 181 pelktipltpvetqdlelatgykvgrcrmekeedlwgspsilsfqtppsapkdvwvs 240
QY 241 NLCGTPGGEPLLLWKAPGCPQVQSVYKVFVWVGGRLESPGEGITCCSLIPSGAEWARVSA 300
Db 241 nlcgtpggeplllwkapgcpvqvsvykvfvwvvggrelspggitccslipsgaewarvsa 300
QY 301 VNATSWEPITNLSLVCLDSASAPRSVAVSSVAGSTELLVWPGPGEPLHVVVDWARDGD 360
Db 301 vnatswepitnlsvlcldsasaprsavassvagsstellvwpgpgeplehvvmdwardgd 360
QY 361 PLEKLNWVRLPGNLSALLPGNFTVGPVYRITVAVSAGLASASSVWGFREELAPLVGP 420
Db 361 pleklnwvrlpgnlsallpgnftvgpvyrityavssaglasassvwgfrelaplvgp 420
QY 421 TLWRQLDAPPGTPTAIWGEVPRHQLRGHLYTHYTLCAQSGTSPSCVMNVSGNTQSVTLPLD 480
Db 421 tlwrqldappgtptaiwgevprrhqlrghlythyltcaqsgtspscvmnvsgntqsvtlpdl 480
QY 481 PNGPCBELWNTASTIAGQGGPPGPIRLHLPDNTLRWKLPGILFLWGLFLGCGLSLATSG 540

Db 481 pwpgeelwvstastagqppgplrlhlpdntlrwkvlpigallfmgllfllgclslatsg 540
Qy 541 RCYHLRHVLPWWWEKVPDPANSSGGOPHMEQVPEAQPLGDLPLILEVEEMEPVPMMESS 600
Db 541 rcyhlrhvlpwwwekvpdpansss-----566
Qy 601 OPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636
Db 567 -----gllgpprpqvla 578

RESULT 5
AA29785
ID AAY29785 standard; Protein; 523 AA.
XX AC
XX AC AAY29785;
XX
XX 04-NOV-1999 (first entry)
XX
XX Partial human DNAX cytokine receptor subunit 1.
XX
KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
KW interleukin B30; DCRS1; DCRS1; IL-B30; cytokine receptor; diagnosis;
KW inflammatory disorder; inflammatory response; innate immunity;
KW morphogenic development; immunological disorder.
XX
XX Homo sapiens.
XX
XX WO9940195-A1.
XX
XX 12-AUG-1999.
XX
XX 05-FEB-1999; 99WO-US02600.
XX
XX 13-MAY-1998; 98US-0078194.
XX 06-FEB-1998; 98US-0073941.
XX
XX (SCHE) SCHERING CORP.
XX
XX Kastelein RA, Matteson JD, McClanahan TK;
XX
XX WPT; 1999-527306/44.
XX N-PSDB; AAZ08867.
XX
XX New receptor subunits useful in the treatment inflammatory disorders
XX
XX Disclosure; Page 10-13; 133pp; English.
XX
XX The present invention describes a composition (I) comprising DNAX
XX cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
XX subunit I (DCRS1) protein, which together encode a new mammalian
XX cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)
XX proteins, or DCRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1
XX is useful for screening for ligands (i.e. agonists/antagonists) from
XX a library of compounds, which are useful for modulating the physiology
XX or development of a cell or tissue culture e.g. inflammatory responses,
XX innate immunity and/or morphogenic development. (R), antibodies and
XX ligands are useful for treatment of conditions, especially immunological
XX disorders, associated with conditions exhibiting abnormal expression of
XX (R). (R) is useful as a phosphate labeling enzyme to label substrates,
XX and the subunits DCRS1 and DCRS1 are useful as immunogens for generating
XX antibodies, or as antigens for binding antibodies. Nucleic acids
XX encoding (R) are useful for identifying related DNAs and mRNAs, and
XX variants from other individuals or species. The present sequence
XX represents the partial human DCRS1, given in the present invention.
XX
XX Sequence 523 AA;

Query Match 82.2%; Score 2875; DB 20; Length 523;
Best Local Similarity 99.6%; Pred. No. 8.9e-217;
Matches 521; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 114 LWPVVFVNLETKOMKNAPRLGPDVDFSEDDPLEATVHAPPTWPSHKVLICQFHYRRCOE 173
Db 1 vwpvfvnletqmkknaprlgpdvdfseddpleatvhwapptwpskhkvilicqfhyrrcqe 60
Qy 174 AAWTLLEPELKTIPITPVEIQDLELATGYKYVGRGRMEKEEDLWGEWSPILSFQTPPPSAP 233
Db 61 aawtllepelktipitpveiqdlatgykyvgrmekeedlwgewspilsfqtppsap 120
Qy 234 KDVTYSGNLCTPGGEEPLLWKAGPCVQVSYKVFVWVGGRRELSPEGITCCCSLIPSGA 293
Db 121 kdvtysgnlctpggeeplllwkapgpcvqvsykwfvwvggrelspegitcccsllipsga 180
Qy 294 EWARVSANVATSWEPILTNLISLVC LDSASAPRSVAVSSISTAGSTELIIVTQPGPELHV 353
Db 181 ewarvsavnatswepltnlslvclldsasaprsavavssistagstceliivtqpgpelehm 240
Qy 354 DWARDGPLEKLNWVRLPPGNLSALLPGNFTGVGPYRITVTAVSASGLASASVWGFREE 413
Db 241 dwardgpleklnwvrlppgnlsallpgnftvgvpyritvtavsaasglasasvvgfree 300
Qy 414 LAPLVGPTLWRLQDAPPGTPAIANGCEVPRHQLRGHLTHYTLCQAQSGTSPSCMVNNGNQ 473
Db 301 laplvgptlwrldappgtpaiangcevrhqlrghlthytltcaqsgtspscmvnngntq 360
Qy 474 SVTLPLDWGPCELWVTASTIAGQGGPPIRLRLHLPDNTLRWKVLPGILFLWGLFLGCG 533
Db 361 svtlpldwgpcelwvtastiaaggppilrlhlpdntlrwkvlpgilflwglflgcg 420
Qy 534 LSLATSGRCYHLRHKVLPWWWEKVPDPANSSGGOPHMEQVPEAQPLGDLPLILEVEEMEP 593
Db 421 lslatsgrcyhlrhkvlpwwwekvpdpansssggophmeqvpeaqplgdlplileveemep 480
Qy 594 PPMESSOPAQATAPLDSGYEKHFLPTPEELGGLGPPRPQVLA 636
Db 481 ppmessopaqataplsgyekhflptpeeigllgpprpqvla 523

RESULT 6
AAW33400
ID AAW33400 standard; Protein; 623 AA.
XX AC
XX AAW33400;
XX
XX 22-MAY-1998 (first entry)
XX
XX Mouse haematopoietic cytokine receptor Zcytor1.
XX
XX Mouse; haematopoietic cytokine receptor; Zcytor1; ligand detection;
XX cancer diagnosis; agonist; antagonist; murine.
XX
XX Mus sp.
XX
XX WO9744455-A1.
XX
XX 27-NOV-1997.
XX
XX 19-MAY-1997; 97WO-US08502.
XX
XX 23-MAY-1996; 96US-0653740.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
XX WPT; 1998-018509/02.
XX N-PSDB; AAT94121.
XX
XX Haematopoietic cytokine receptor - useful for ligand detection, and
XX pathological condition diagnosis
XX
XX Claim 3; Pages 54-58; 86pp; English.
XX

CC The present sequence is the mouse haematopoietic cytokine
 CC receptor Zcytor1, useful for ligand detection, and pathological
 CC condition diagnosis, including cancer. Receptor agonists of the
 CC protein can be used to stimulate the proliferation and development
 CC of target cells in vitro and in vivo. The agonists can stimulate
 CC cell mediated immunity and lymphocyte proliferation, to treat
 CC infection involving immunosuppression, e.g. viral infections. They
 CC may also be used to suppress tumours, induce cytotoxicity, treat
 CC leukopenias and enhance the regeneration of the T-cell repertoire
 CC after bone marrow transplantation. Antagonists of the protein may
 CC be used to suppress the immune system, treat autoimmune diseases,
 CC including rheumatoid arthritis, multiple sclerosis and diabetes,
 CC mellitis. Immune suppression caused by the antagonists can also be
 CC used to reduce rejection of tissue or organ transplants and grafts,
 CC and to treat T-cell specific leukaemias and lymphomas.

XX Sequence 623 AA;

3; Gaps 8; Indels 161; Mismatches 61; Pred. No. 1.3e-151; Score 2044; DB 19; Length 623;

3; Gaps 8; Indels 161; Mismatches 61; Pred. No. 1.3e-151; Score 2044; DB 19; Length 623;

QY 14 LPKALLPLLVLFQTRPGGAGPLQCVGCPGLDGLNCSWEPLDGLGAPSELHLSQSKY 73
 Db 9 ltpcllellsalmllgtrphgspglqcyvsgplglneswepldgletppvlyhqskqy 68
 QY 74 RSNKQTQVAAGRSWVAIPROQLTMSDKLLVMGTKAGOPLPWPFPVFNLETKMKNAPRL 133
 Db 69 hpnrvewkvpqskqwtlpreqftmadkllwgkqgrplwssvsnletqmkpdtqj 128
 QY 134 GPDVDFSEDDPLEATVHMAPTWPSHKVILICQFHYRRCQAAWTLLEPELKTIPLPVBI 193
 Db 129 fsqvdiseateatqwpvvpqakltcfrykecaqeatwrllepqlktdgtvpem 188
 QY 194 QDLELATGKYVGRCHMEKEEDLWGEWSILSFQTPPPSAPKDVWVSGNLCTGPGGEEPLL 253
 Db 189 qllepqtcyvsgvqevngyp-wgevsyplsfqtpdpedvwsygtvcetsgkraall 247
 QY 254 LMKAGPCVQVSQVYKVMFWGGRPLSPGEGITCCSLIPSGAEWARVSAVNATSWEPITNLS 313
 Db 248 vnkdrpcqvtytwfagaditttqeepvckspvpawmewavspgnstswvptnls 307
 QY 314 LVCLDSASAPRSVAVSSVSIAGSTELLVWQPGGEPLEHVVDWARGDPLEKLNWVRLPPG 373
 Db 308 lvcldesapcdvgvssadgsqikvtrkqgrkpleyvvdwaqgdslckinwtrlpbg 367
 QY 374 NLSALLPGNFTVGVPIRITVAVSAGSLASASSVWGFEELAPLPGPTLWRLQDAPPGNP 433
 Db 368 nstllpgfkgvpyrictvay99glaapsvwgfrelvplagpavwripddppgcp 427
 QY 434 ATAWGEVPRHQLRGLHLYTLCAQSGTSPVCMNVSGNTQSVTLPLDPLWGPCELWYAST 493
 Db 428 vvawgevprhqlrgathqthfclqsrqlstvcnrvssqqtatlpnlhsgsfklwvtst 487
 QY 494 IAGQGGPGLRLHLPDNLTKVLPGLILFNLGLFLGLGCLSLATS-GRCYHLRHVKV 549
 Db 488 vagqggppgdlslhpdnrlrkaipwflslgillmgcglslastrclqarclhrwlk1 547
 QY 550 LPRWWEKVPDPANSSGQPHMFOYPEAQPLGLDPLTLEVEEMPPVMESSQPAQATPL 609
 Db 548 lpgqtwervpdpanssgpkykelsvpqpkdgpplveeveelgvves---pkasapl 604
 QY 610 DSGYKHEFLPTPEELGLL 627
 Db 605 ysagkehflptpeeigl1 622

RESULT 7
 AAU01854
 ID AAU01854 standard; Protein; 623 AA.
 XX
 AC AAU01854;

XX 07-SEP-2001 (first entry)
 DT Mouse type I cytokine receptor, mTCCR.
 XX
 DE Mouse type I cytokine receptor; TCCR; T-cell differentiation;
 KW Th1; Th2; agonist; antagonist; autoimmune inflammatory disease;
 KW allograft rejection; multiple sclerosis; inflammatory bowel disease;
 KW insulin-dependent diabetes mellitus; infectious disease;
 KW human immunodeficiency virus; allergic disorder; asthma;
 KW allergic rhinitis; HIV.
 XX
 OS Mus musculus.
 XX
 FH Key
 FT Peptide
 FT /label= Signal_peptide
 FT 1..24
 FT Modified-site
 FT 10..13
 FT /note= "Casein kinase II phosphorylation site"
 FT 14..51
 FT Region
 FT /note= "Region of homology to human erythropoietin"
 FT 25..623
 FT Protein
 FT /label= Mature_mTCCR
 FT 36..49
 FT Region
 FT /note= "Cytokine receptor family signature 1"
 FT 43..48
 FT Modified-site
 FT /label= N_myristoylation_site
 FT 46..49
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT 93..96
 FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 102..102
 FT Modified-site
 FT /label= N_myristoylation_site
 FT 130..133
 FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 172..175
 FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 184..187
 FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 202..209
 FT Modified-site
 FT /note= "Tyrosine kinase phosphorylation site"
 FT 211..219
 FT Region
 FT /note= "Region of homology with murine
 FT Interleukin-5 receptor"
 FT 235..238
 FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 240..245
 FT Modified-site
 FT /label= Amidation_site
 FT 271..274
 FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 272..275
 FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 295..300
 FT Modified-site
 FT /label= N_myristoylation_site
 FT 296..299
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT 305..308
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT 321..326
 FT Modified-site
 FT /label= N_myristoylation_site
 FT 323..326
 FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 330..335
 FT Modified-site
 FT /label= N_myristoylation_site
 FT 360..361
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT 367..372
 FT Modified-site
 FT /label= N_myristoylation_site
 FT 368..371
 FT Modified-site
 FT /note= "Asn is N-glycosylated"
 FT 393..398
 FT Modified-site
 FT /label= N_myristoylation_site
 FT 461..464
 FT Modified-site

Key Location/Qualifiers
Peptide 1..24
Protein /label= signal peptide
Region /label= human G-CSF receptor
FT /label= transmembrane region
FT /note= "putative"

W09105046-A.
18-APR-1991.
24-SEP-1990; 90WO-0005434.
03-APR-1990; 90US-0522952.
26-SEP-1989; 89US-0412816.
03-OCT-1989; 89US-0416306.
IMMU-) IMMUNEX CORP.
Smith CA, Larsen AD, Curtis BM;
WPI: 1991-132853/18.
N-PSDB; AAQ11579.
Granulocyte-colony-stimulating factor (G-CSF) receptor DNA and protein - useful as diagnostics and for regulating immune and inflammatory responses
Disclosure: Fig 2,3,4,5; 34pp; English.
A cDNA library was constructed from cytoplasmic placental poly(A)+ RNA. Purified cDNA fragments were cloned into pSfCAV vector for transformation into E.coli DH5 strain alpha. Transformants were plated to provide approximately 800 colonies per plate. The colonies were harvested and each pool used to prepare plasmid DNA for transfection into COS-7 cells. Transformants expressing biologically active cell surface G-CSFR were identified by screening for ability to bind 125-Iodine-G-CSF. Bacteria from a positive pool were plated and plasmids prepared. COS-7 cells were transfected and a single positive clone was identified and designated D-7. The deduced amino acid sequence of the G-CSFR it encodes, is shown.
See also AAQ11580.
Sequence 783 AA;

Local Similarity 8.5%; Score 298.5; DB 12; Length 783;
Matches 160; Conservative 75; Mismatches 250; Indels 227; Gaps 34;

50 LNCSEPLDGLGAPSELHLQSQYRSN-KTQTVAV-----AAGRSWVAIPREQLTMSDKL 103
140 lloqewpgpethlptstftksfksrncctqgdsildcvpkdgdshcciprkhllyqnm 199
104 LWN-----GTRKAGPLW-----PPVFVNLETKMKNAPRLG-----PDVDF 139
200 giwvqaenaigtmspqclcdmdvvkllppmlrntmdpspeaappqagclqicwep--- 255
140 SEDDPLEATVHNAWPTWPSKVKLICOF-HYRCQEAATWLLPELXTIPTVPEIQDLLEL 198
256 -----wqpglhinqk---celrhkprgeaswalvgp-----lplealqyel 294
199 -----ATGKYVYGRCRMKEEDLWGSWSPILSFQTPPSAPK---DVWVSGNLCGTPGGEE 250
295 cgltpataytlqircirwlpghwsdwspslelrteraptvrltdw----- 341
251 PLLLMKPGPCVQVYKVFVWVGGRLESPGEGITCCCLIPSGAEWARSAVNATSWEP-- 308
342 ----wrg-----rqldprtvqlfwkvpvleedsgriqgy-vvswrpsg 379
309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335

Db 380 qagailplcnttelstcfhlhpseagevalvaynsagtsrptpvfisesrgpaltrihama 439
QY 336 ----ELLVTWQPCGPEPLEHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGV 388
Db 440 rdphslwvgwepnpwpvggyviewlgppsaansnktwrmeqngratgflikenirpfql 499
QY 389 YRITITAVSASGLASASSVMGFREELAPLVGPTLMRLQDAPPCTAIAWGEVPRHOLRGH 448
Db 500 yeiivtplyqdtmgpsqhvayseqmapshapel-hlkhightwaqlwvpeppelgksp 558
QY 449 LTHYTLCAQSGTSPSVMNVSGNTSVTLPLDLPWGPCELV-----VTA 491
Db 559 lthytifwnaqnqsfailnassrgfvihgle--paslyhihlmaasqagatnstvlcl 616
QY 492 STTAGOGPPGPIRLRLHLPDNTLRWVLPGLFLWGLFL--CGGLSLATSGRCYHLRHK 548
Db 617 mcltpegs-----elh-----ilgflgllllltclcg-----tawlcspnrk 655
QY 549 VLPRWVWEKVPDPANSSG-----QPHMEQVP--EAQPLGDLPILEVEEMEPPP--- 595
Db 656 ---nplwpsvpdpahsslgswvptimeedafqlpglgtptpckltvleedekkpvpwesh 712
QY 596 -----VMSSQPAQATAP-LDSGYEKHFLPTPEELGLGPPR 631
Db 713 nssetcglptlvqtyvlqgdpravstqpgsg-----tsdq-----agppr 754

RESULT 12
AAR77868
ID AAR77868 standard; Protein; 783 AA.
XX
AC AAR77868;
DT 15-NOV-1995 (first entry)
XX Human placental G-CSFR.
KW G-CSFR; G-CSF; granulocyte-colony stimulating factor receptor.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..23
FT /label= sig_peptide
FT Domain 628..653
FT /label= Transmembrane_domain
XX
PN US5422248-A.
XX
PD 06-JUN-1995.
XX
PF 26-SEP-1989; 89US-0412816.
XX
PR 24-SEP-1990; 90US-0587329.
PR 26-SEP-1989; 89US-0412816.
PR 03-OCT-1989; 89US-0416306.
PR 03-APR-1990; 90US-0522952.
PR 15-JAN-1993; 93US-0006183.
XX
PA (IMMU) IMMUNEX CORP.
XX
PI Curtis BM, Larsen AD, Sims JE, Smith CA;
XX
DR WPI: 1995-214655/28.
DR N-PSDB; AAQ95481.
XX
PT New DNA encoding granulocyte-colony stimulating factor receptors
PT useful for prodn. of G-CSFR which is used to attenuate immune
XX responses
XX
PS Disclosure: Fig. 2A-C; 16pp; English.
XX

[illegible]

```

Db 342 -----wrq-----rqlprtqlfwkvpbleedsgrlqgy-vvswrpsg 379
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335
Db 380 qagallplcmtelstctfhlpsaeqavalvaynsagtsrtpvfvfesrgpaltrihama 439
QY 336 -----ELLVTWQPGPGPLEHVVDWARDGPLEKLN--WVRLPPGNLSA--LLPGNFTVGVY 388
Db 440 rdphslwvgwepnpwpqgyvlewglgppsasnsnktwrmeqngratgflkenirpfql 499
QY 389 YRITVTAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPGCTPAIANGVPRHQLRGH 448
Db 500 yeiivtplyqdtmgsqhvayysqemapshapel-hlkhightwaqlwvpeppelgksp 558
QY 449 LTHYTLCAQSGTSPSVCNMVSGNTQSVTLDPDLPWGPCELW-----VTA 491
Db 559 lthytifwtanqqsfsallnassrgfvlhgile--paslyhihlmaasqagatnstvltl 616
QY 492 STIAGGPGPILRLHLPDNTLRWKVLPGLFLWGLFLL--GCGLSLATSGRCYHLRHK 548
Db 617 mltltpgs-----elhi-----ilglfllllltclcg----tawlcspnrk 655
QY 549 VLPRTWWEKVPDPANSSG-----QPHMEQVP--EAQPLGDLPTLEVEEMEP-- 595
Db 656 ----nplwpsvdpahsigswwptimeedafqlpglgtpttkltvleedekkpwpwesh 712
QY 596 -----YMSSQPAQATAP-LDSGYEKHFLPTPEELGLLGPPR 631
Db 713 nssetcglptlvqtylqgdpravstcqsqsq-----tsdq---agppr 754

RESULT 14
AAW10486
ID AAW10486 standard; Protein; 800 AA.
XX
AC AAW10486;
XX
XX
XX 27-APR-1997 (first entry)
XX Human granulocyte colony stimulating factor receptor.
XX Granulocyte colony stimulating factor receptor; G-CSFR; diagnosis;
XX therapy.
XX Homo sapiens.
XX Location/Qualifiers
XX Key 1..24
XX Peptide /label= Sig_peptide
XX Protein 25..783
XX /label= Mat_protein
XX Domain 628..653
XX /label= Transmembrane_domain
XX Misc-difference 750..800
XX /note= "alternative C-terminal sequence"
XX
XX US5589456-A.
XX
XX 31-DEC-1996.
XX
XX 26-SEP-1989; 89US-0412816.
XX
XX 24-SEP-1990; 90US-0587329.
XX 26-SEP-1989; 89US-0412816.
XX 03-OCT-1989; 89US-0416306.
XX 03-APR-1990; 90US-0522952.
XX 15-JAN-1993; 93US-0006183.
XX 02-FEB-1985; 95US-0382771.
XX (IMV ) IMMUNEX CORP.
XX
XX Curtis KM, Larsen AD, Sims JE, Smith CA;
XX

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DR WPI; 1997-076879/07.
DR N-PSDB; AAT47100.
XX
XX Recombinant granulocyte colony stimulating factor receptor - for
PT diagnostic, therapeutic and research uses
XX
XX Claim 1; Fig 3; 15pp; English.
XX
XX An alternative form (AAW10486) of human granulocyte colony
CC stimulating factor receptor (G-CSFR) (see also AAW10485) results
CC from alternative splicing and a change in the reading frame,
CC leading to a different C-terminal amino acid sequence. It is the
CC product of a cDNA clone (AAT47100) isolated from a human placental
CC library. Recombinant G-CSFRs, esp. soluble forms comprising the
CC extracellular domain, or modified forms having inactivated
CC N-glycosylation sites, altered KEX2 protease cleavage sites or
CC conservative amid acid substns., can be produced in host cells.
CC G-CSFR polypeptides are useful in diagnostic assays of G-CSF, and
CC for raising antibodies of use in diagnosis and therapy. G-CSFR
CC can also be used in therapy to bind or scavenge G-CSF.
XX
XX Sequence 800 AA;
XX
XX Query Match 8.5%; Score 297.5; DB 18; Length 800;
XX Best Local Similarity 22.8%; Pred. No. 9e-15;
XX Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;
XX
QY 50 LNCSEPLDGLCAPSELHLQSKYRSN-KTQIVAV-----AAGRSWVAIPRQLTMSDKL 103
Db 140 llicqewpethlptsftlksfksrgnoqtgqdsldcvpkdgqshcciprkhllyqnm 199
QY 104 LVW-----GTKAGQPLW-----ppVFVNLETMQKNAPRLG-----PDVDF 139
Db 200 glwvqaenalgtmspqicldgmdvkvkleppmlrmdpapeaappqagclqlwep--- 255
QY 140 SEDDPLEATVHWAPPTWPSHKVLICQF-HYRCQBAWTLLEPELKTPLTPVEQDLEL 198
Db 256 -----wqpglhinqk---celrhkpkrgaeaswalvgp-----lplealqyel 294
QY 199 ----ATGVKVGRCRMEKEEDLWGEWSPILSFQTPPPSAPK--DWVSGNLCGTPGGE 250
Db 295 cglipataytlqiclrwplghwsdpslelrtrteraptvrltdw----- 341
QY 251 PLLLWKAPGCVQSVKYVFWVGGRELSPEGITCCCLIPSGAEWARVSAVNATSWEP-- 308
Db 342 ----wrq-----rqlprtqlfwkvpbleedsgrlqgy-vvswrpsg 379
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335
Db 380 qagallplcmtelstctfhlpsaeqavalvaynsagtsrtpvfvfesrgpaltrihama 439
QY 336 ----ELLVTWQPGPGPLEHVVDWARDGPLEKLN--WVRLPPGNLSA--LLPGNFTVGVY 388
Db 440 rdphslwvgwepnpwpqgyvlewglgppsasnsnktwrmeqngratgflkenirpfql 499
QY 389 YRITVTAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPGCTPAIANGVPRHQLRGH 448
Db 500 yeiivtplyqdtmgsqhvayysqemapshapel-hlkhightwaqlwvpeppelgksp 558
QY 449 LTHYTLCAQSGTSPSVCNMVSGNTQSVTLDPDLPWGPCELW-----VTA 491
Db 559 lthytifwtanqqsfsallnassrgfvlhgile--paslyhihlmaasqagatnstvltl 616
QY 492 STIAGGPGPILRLHLPDNTLRWKVLPGLFLWGLFLL--GCGLSLATSGRCYHLRHK 548
Db 617 mltltpgs-----elhi-----ilglfllllltclcg----tawlcspnrk 655
QY 549 VLPRTWWEKVPDPANSSG-----QPHMEQVP--EAQPLGDLPTLEVEEMEP-- 599
Db 656 ----nplwpsvdpahsigswwptimeedafqlpglgtpttkltvleedekkpwpwesh 711
QY 600 SQPAQATAPLDSGYEKHFLPTPEELGLL-GPPR 631

```

Db 712 hnssetcg-----lptlvqtylqgdpr 734

RESULT 15
AAR11742
ID AAR11742 standard; Protein: 801 AA.

AC AAR11742;
DT 04-JUL-1991 (first entry)
DE Clone 25-1 encoded human G-CSF receptor.
KW granulocyte colony stimulating factor; receptor; clone 25-1.
OS Homo sapiens.

Key Location/Qualifiers
1..24
Peptide /label= signal peptide
25..801
Protein /label= human G-CSFR

PN W09105046-A.
PD 18-APR-1991.
PF 24-SEP-1990; 90WO-0005434.
PR 03-APR-1990; 90US-0522952.
PR 26-SEP-1989; 89US-0412816.
PR 03-OCT-1989; 89US-0416306.

PA (IMMU-) IMMUNEX CORP.
PI Smith CA, Larsen AD, Curtis BM;
WPI; 1991-132853/18.
N-PSDB; AAQ11580.

Granulocyte-colony-stimulating factor (G-CSF) receptor DNA and protein - useful as diagnostics and for regulating immune and inflammatory responses
Disclosure; Fig 2,3,4,5,6; 34pp; English.

This is the deduced amino acid sequence of the G-CSFR encoded by clone 25-1. The C-terminal differs from that encoded by clone D-7 due to an alternative splicing arrangement. The protein can be used in compositions for use in therapy, diagnosis, assay of G-CSFR, or in raising antibodies to G-CSFR.
See also AAQ11579.

Sequence 801 AA;

Query Match 8.5%; Score 297.5; DB 12; Length 801;
Best Local Similarity 22.8%; Pred. No. 9e-15;
Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;
Qy 50 LNCSEWELGDLGAPSELHLSQKYSRN-KTQTVAV-----AAGRSWAIPREQLTMSDKL 103
Db 140 llicwepgpethptsftlksfsgnqctgdsildecvpkdgshcciprkhillyqnm 199
Qy 104 LWV-----GKAGQPLW-----PPVFVNLETQMKPNAPRLG-----PDVDF 139
Db 200 giwvgaenalgtmspgicldpmdvkvkleppmlrtmdpspeaappqagclqlcwep---- 255
Qy 140 SEDDPLEATVWAPPTWPSHKVLICQF-HYRRCOEAAWTLLEPELKTPTLPVEIQDLEL 198
Db 256 -----wbp9llhinqk---celrhkprgeaswalvgp-----lplealgyel 294

Qy 199 -----ATGYKVYGRCRMKEEDLWGEWSPILSFQPPSAPK---DWVWSGNLCGTPGGEE 250
Db 295 cglipataytlqircirwplpghwsdpslelrtrteraptvrltdw----- 341
Qy 251 PLLLWKAFCPCQVQSYKVFVWVGGRGELSPEGITCCSLIPSGAEWARYSAVNATSWEP-- 308
Db 342 ----wrq-----rqlprrvtqlfwkpvpleedsgriqgy-vvswrpsg 379
Qy 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSISAGST----- 335
Db 380 qagailplcncntelctfhlpseaqeavalvaynsagtsrptpvfseesgpaltrihama 439
Qy 336 ----ELLVTVQPGCEPLEHVVDWARDGDPLEKLN--WVRLPPGNLSA--LLPGNFTVGV 388
Db 440 rdphslwgvwepnpwpggyvlewdlgppssansnktwrmegngratgflikenirpfql 499
Qy 389 YRITVTAVSASGLASASSVMGFRRELAPLVGPTLWRLQDAPPCTPAIANGVEVPRHQLRGH 448
Db 500 yeiivtplyqdtmgpsqhvayysgemapshapel-hlkhgktwaqlwvpeppelgksp 558
Qy 449 LTHYTLCAGSGTSPSCVMNVSGNTQSVTLPDLPWGPCELW-----VTA 491
Db 559 lthytfwnaqqsfailnassrgfvlhgile--paalyhihlmaasagagatnstvitl 616
Qy 492 STIAGQGPPGPIRLUHLDPDNTLRWKVLPGLFLWGLFL--GCGLSLATSGRCYHLRHK 548
Db 617 mltltpesg-----elhi-----ilglflllllclcg-----tawlcspnrk 655
Qy 549 VLPWRWVEKVPDPANSSSG-----QPHMEQVP--EAQPLGDLPILEVEEMEPPVMES 599
Db 656 ---nplwpsvpopahsslgswvptimeedafqlpglgtpttkltvleedekkkvp-wes 711
Qy 600 SQPAQATAPLDSGYEKHFELPTPEELGLL-GPPR 631
Db 712 hnssetcg-----lptlvqtylqgdpr 734

Search completed: May 9, 2002, 06:06:12
Job time: 144 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:03:48 ; Search time 24.01 Seconds
(without alignments)
596.089 Million cell updates/sec

Title: US-09-692-504-1

Perfect score: 3498

Sequence: 1 MRGGGAPFWLPLKALL.....FLTPPELGLGPPRPQVLA 636

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3498	100.0	636	1	US-08-653-740-5
2	3498	100.0	636	2	US-09-073-594-5
3	3498	100.0	636	3	US-09-275-925-5
4	3150	90.1	578	1	US-08-653-740-3
5	3150	90.1	578	2	US-09-073-594-3
6	3150	90.1	578	3	US-09-275-925-3
7	2044	58.4	623	1	US-08-653-740-7
8	2044	58.4	623	2	US-09-073-594-7
9	2044	58.4	623	3	US-09-275-925-7
10	380	10.9	862	2	US-08-685-118-2
11	380	10.9	862	2	US-08-915-495-2
12	380	10.9	862	2	US-08-914-520-2
13	298.5	8.5	783	6	5422248-2
14	297.5	8.5	836	1	US-07-923-976-4
15	294.5	8.4	602	2	US-08-419-652-6
16	292	8.3	863	1	US-07-923-976-8
17	277	7.9	837	1	US-07-923-976-2
18	268.5	7.7	771	1	US-07-923-976-6
19	248	7.1	708	1	US-07-797-556-2
20	248	7.1	708	1	US-08-308-881-2
21	248	7.1	708	2	US-09-058-463-2
22	248	7.1	708	2	US-09-059-099-2
23	248	7.1	708	3	US-09-058-264-2
24	248	7.1	708	5	PCT-US95-06530-2
25	247	7.1	918	2	US-08-825-558-6
26	236.5	6.8	572	2	US-08-419-652-5
27	226	6.5	979	1	US-08-308-881-6

28	226	6.5	979	2	US-09-058-263-6	Sequence 6, Appli
29	226	6.5	979	2	US-09-059-099-6	Sequence 6, Appli
30	226	6.5	979	3	US-09-058-264-6	Sequence 6, Appli
31	226	6.5	979	5	PCT-US95-06530-6	Sequence 6, Appli
32	210	6.0	658	2	US-08-825-558-4	Sequence 4, Appli
33	206.5	5.9	1097	1	US-07-943-843-6	Sequence 6, Appli
34	206.5	5.9	1097	1	US-08-347-003-6	Sequence 6, Appli
35	205	5.9	1001	1	US-07-797-556-6	Sequence 6, Appli
36	205	5.9	1001	1	US-07-943-843-2	Sequence 2, Appli
37	205	5.9	1001	1	US-08-347-003-2	Sequence 2, Appli
38	199	5.7	620	2	US-08-419-652-7	Sequence 7, Appli
39	178.5	5.1	885	1	US-08-372-892-4	Sequence 4, Appli
40	178	5.1	894	1	US-08-372-892-2	Sequence 4, Appli
41	178	5.1	894	1	US-08-445-640-34	Sequence 34, Appli
42	178	5.1	894	3	US-08-170-558-34	Sequence 34, Appli
43	178	5.1	894	3	US-08-447-314-34	Sequence 34, Appli
44	178	5.1	894	3	US-08-445-461-34	Sequence 34, Appli
45	172	4.9	1711	2	US-08-342-930-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-653-740-5
; Sequence 5, Application US/08653740
; Patent No. 5792850
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc. East
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,740
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-653-740-5

Query Match 100.0%; Score 3498; DB 1; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.7e-280;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGGGAPFWLPLKALLPLLVLFQTRPQGSAGPLQCYGVGLDNCWEPLGDL 60

Db 1 MRGGGAPFWLPLKALLPLLVLFQTRPQGSAGPLQCYGVGLDNCWEPLGDL 60

ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,925
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-275-925-5

Query Match 100.0%; Score 3498; DB 3; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.7e-280;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGRGAPFWLWPLPKLALLPQLVLFQTRPQGSAGPLQCYGVGVLGDLNCSWEPLGDL 60
Db 1 MRGRGAPFWLWPLPKLALLPQLVLFQTRPQGSAGPLQCYGVGVLGDLNCSWEPLGDL 60
Qy 61 GAPSELHLSQSKYRSNKTQTVAAGRSWVAIPREOLTMDSKLLVWGTAKGQPLWPPVFV 120
Db 61 GAPSELHLSQSKYRSNKTQTVAAGRSWVAIPREOLTMDSKLLVWGTAKGQPLWPPVFV 120
Qy 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
Db 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
Qy 181 PELKTIPTLTPVEIQDELATGYKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
Db 181 PELKTIPTLTPVEIQDELATGYKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
Qy 241 NLCGTPGGEPLLLWKAPGPCVQVSYKVFVWVGRELSPGEGITCCSLIPSGAENARVSA 300
Db 241 NLCGTPGGEPLLLWKAPGPCVQVSYKVFVWVGRELSPGEGITCCSLIPSGAENARVSA 300
Qy 301 VNATSWEPLTNLSVLCDLSASAPRSVAVSSVYTAGSTELLVTPQGPGEPLHVVDNARDGD 360
Db 301 VNATSWEPLTNLSVLCDLSASAPRSVAVSSVYTAGSTELLVTPQGPGEPLHVVDNARDGD 360
Qy 361 PLEKLNWVRLPPGNLSALLPQNFVGVYRITVTAVSAGSLASASSVWGFRLEAPLVGP 420
Db 361 PLEKLNWVRLPPGNLSALLPQNFVGVYRITVTAVSAGSLASASSVWGFRLEAPLVGP 420
Qy 421 TLWRLODAPPGTATAGQPPGPIRLHLDPDNTLRMKVLPGLILFWGLFLGCGLSLATSG 480
Db 421 TLWRLODAPPGTATAGQPPGPIRLHLDPDNTLRMKVLPGLILFWGLFLGCGLSLATSG 480
Qy 481 PWGCELVWTAATAGQPPGPIRLHLDPDNTLRMKVLPGLILFWGLFLGCGLSLATSG 540
Db 481 PWGCELVWTAATAGQPPGPIRLHLDPDNTLRMKVLPGLILFWGLFLGCGLSLATSG 540
Qy 541 RCYHLRHKVLPVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPTILEVEEMEPVWVMESS 600
Db 541 RCYHLRHKVLPVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPTILEVEEMEPVWVMESS 600

Db 541 RCYHLRHKVLPVWWEKVPDPANSSSQPHMEQVPEAQPLGDLPTILEVEEMEPVWVMESS 600
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLLGPVLA 636
Db 601 QPAQATAPLDSGYEKHFLPTPEELGLLGPVLA 636
RESULT 4
US-08-653-740-3
Sequence 3, Application US/08653740
Patent No. 5792850
GENERAL INFORMATION:
APPLICANT: James W. Baumgartner
APPLICANT: Donald C. Foster
APPLICANT: Frank J. Grant
APPLICANT: Cindy A. Sprecher
TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,740
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-740-3

Query Match 90.1%; Score 3150; DB 1; Length 578;
Best Local Similarity 90.9%; Pred. No. 7.7e-252;
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

Qy 1 MRGRGAPFWLWPLPKLALLPQLVLFQTRPQGSAGPLQCYGVGVLGDLNCSWEPLGDL 60
Db 1 MRGRGAPFWLWPLPKLALLPQLVLFQTRPQGSAGPLQCYGVGVLGDLNCSWEPLGDL 60
Qy 61 GAPSELHLSQSKYRSNKTQTVAAGRSWVAIPREOLTMDSKLLVWGTAKGQPLWPPVFV 120
Db 61 GAPSELHLSQSKYRSNKTQTVAAGRSWVAIPREOLTMDSKLLVWGTAKGQPLWPPVFV 120
Qy 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
Db 121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRCQEAATLLE 180
Qy 181 PELKTIPTLTPVEIQDELATGYKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
Db 181 PELKTIPTLTPVEIQDELATGYKYVGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSG 240
Qy 241 NLCGTPGGEPLLLWKAPGPCVQVSYKVFVWVGRELSPGEGITCCSLIPSGAENARVSA 300
Db 241 NLCGTPGGEPLLLWKAPGPCVQVSYKVFVWVGRELSPGEGITCCSLIPSGAENARVSA 300

QY 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSIAGSTELLVTWQPGPELHVVDWARDGD 360
DB 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSIAGSTELLVTWQPGPELHVVDWARDGD 360
QY 361 PLEKLNWRLPPGNLSALLPGNETVGVYRITVTAVSASGLASSVWGMFRELAPLVGP 420
DB 361 PLEKLNWRLPPGNLSALLPGNETVGVYRITVTAVSASGLASSVWGMFRELAPLVGP 420
QY 421 TLWLQDAPPPTAIAMGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLPLDL 480
DB 421 TLWLQDAPPPTAIAMGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLPLDL 480
QY 481 PWGPELWVTASTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLLGCGLSLATSG 540
DB 481 PWGPELWVTASTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLLGCGLSLATSG 540
QY 541 RCYHLRHKVLPKRWWEKVPDPANSSSQPHMEQVPEAQPLGLDLPILVEEMEPVWNESS 600
DB 541 RCYHLRHKVLPKRWWEKVPDPANSSSQPHMEQVPEAQPLGLDLPILVEEMEPVWNESS 600
QY 601 QPAQATAPLDSGYEKHFLPTPELGLGPPRPQVLA 636
DB 567 -----GLLGPPRPQVLA 578

RESULT 5
US-073-594-3
; Sequence 3, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-073-594-3

Query Match 90.1%; Score 3150; DB 2; Length 578;
Best Local Similarity 90.9%; Pred. No. 7.7e-252;
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

QY 1 MRGCGAPFWLWPLPKLALLPLLWVLFQRTPOGSAGPLQCYGVGPLGDLNCSWEPLGDL 60
DB 1 MRGCGAPFWLWPLPKLALLPLLWVLFQRTPOGSAGPLQCYGVGPLGDLNCSWEPLGDL 60
QY 61 GAPSELHLQSQKRYRKNKTQTVAAAGRSWVAIPREOLTMDSKLLVMGTAKAGQPLWPPVFV 120
DB 61 GAPSELHLQSQKRYRKNKTQTVAAAGRSWVAIPREOLTMDSKLLVMGTAKAGQPLWPPVFV 120
QY 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQHFHYRRCQEAATLLE 180
DB 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPPTWPSHKVLICQHFHYRRCQEAATLLE 180
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DB 181 PELKTIPLTPVETQDLELATGYKYVGRCKMEKEEDLWGEWSPILSFQTTPPSAPKDVWVSG 240
QY 241 NLGCTPGGEEPLLWKAPGCVQVSYKVMFWGRELSPGITCCCSLIPSGAEWARSVA 300
DB 241 NLGCTPGGEEPLLWKAPGCVQVSYKVMFWGRELSPGITCCCSLIPSGAEWARSVA 300
QY 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSIAGSTELLVTWQPGPELHVVDWARDGD 360
DB 301 VNATSWEPNLNLSVCLDSASAPRSVAVSSIAGSTELLVTWQPGPELHVVDWARDGD 360
QY 361 PLEKLNWRLPPGNLSALLPGNETVGVYRITVTAVSASGLASSVWGMFRELAPLVGP 420
DB 361 PLEKLNWRLPPGNLSALLPGNETVGVYRITVTAVSASGLASSVWGMFRELAPLVGP 420
QY 421 TLWLQDAPPPTAIAMGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLPLDL 480
DB 421 TLWLQDAPPPTAIAMGEVPRHQLRGHLTHYTLCAQSGTSPSCMVNVSNTQSVTLPLDL 480
QY 481 PWGPELWVTASTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLLGCGLSLATSG 540
DB 481 PWGPELWVTASTIAGOGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLLGCGLSLATSG 540
QY 541 RCYHLRHKVLPKRWWEKVPDPANSSSQPHMEQVPEAQPLGLDLPILVEEMEPVWNESS 600
DB 541 RCYHLRHKVLPKRWWEKVPDPANSSSQPHMEQVPEAQPLGLDLPILVEEMEPVWNESS 600
QY 601 QPAQATAPLDSGYEKHFLPTPELGLGPPRPQVLA 636
DB 567 -----GLLGPPRPQVLA 578

RESULT 6
US-09-275-925-3
; Sequence 3, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-275-925-3

Query Match 90.1%; Score 3150; DB 3; Length 578;
Best Local Similarity 90.9%; Pred. No. 7.7e-252;
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

1 MRGGAGFWMPLPKLALLPLLWLFQTRPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
1 MRGGAGFWMPLPKLALLPLLWLFQTRPQGSAGPLQCYGVGPGDLNCSWEPLGDL 60
Qy 61 GAPSELHLSQKYSRKNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPPV 120
Db 61 GAPSELHLSQKYSRKNKTQTVAAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPPV 120
Qy 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPTPWPSHKVLICOFHYRRCOEAAWTLLE 180
Db 121 NLETKMKNAPRLGPDVDFSEDDPLEATVHWAPTPWPSHKVLICOFHYRRCOEAAWTLLE 180
Qy 181 PELKTIPTVPEIQDELATGYKYVGRCMKEEDLWSEWSPILSFQPPSPAKDVWVSG 240
Db 181 PELKTIPTVPEIQDELATGYKYVGRCMKEEDLWSEWSPILSFQPPSPAKDVWVSG 240
Qy 241 NLCTPGGEEPLLLWKAPCPQVQSYKVFVWGGRELSPEGITCCSLIPSGAEWARVSA 300
Db 241 NLCTPGGEEPLLLWKAPCPQVQSYKVFVWGGRELSPEGITCCSLIPSGAEWARVSA 300
Qy 301 VNATSWPEPLNLSLVCLDSASAPRSVAVSSVWGGRELSPEGITCCSLIPSGAEWARVSA 360
Db 301 VNATSWPEPLNLSLVCLDSASAPRSVAVSSVWGGRELSPEGITCCSLIPSGAEWARVSA 360
Qy 361 PLEKLNWVRLPPGNLSALLPQNTVGVYRITVAVSAGLSASVWGFREELAPLVGP 420
Db 361 PLEKLNWVRLPPGNLSALLPQNTVGVYRITVAVSAGLSASVWGFREELAPLVGP 420
Qy 421 TLWRLODAPPGTATAMGEVPRHQLRGLHLYTLCAQSGTSPSVCMNYSNGTQSVTLPLD 480
Db 421 TLWRLODAPPGTATAMGEVPRHQLRGLHLYTLCAQSGTSPSVCMNYSNGTQSVTLPLD 480
Qy 481 PWGPELVWVTAAGQPPGPIRLHLPDNTLRKVLPGILFLWGLFLLGGLSLATSG 540
Db 481 PWGPELVWVTAAGQPPGPIRLHLPDNTLRKVLPGILFLWGLFLLGGLSLATSG 540
Qy 541 RCYHLRHKVLRVWKEVDPDANSSGQPHMEQVPEAQLGDLPLILEVEEMEPVPMESS 600
Db 541 RCYHLRHKVLRVWKEVDPDANSSGQPHMEQVPEAQLGDLPLILEVEEMEPVPMESS 600
Qy 601 QPAQATAPLDSGYEKHFLPTPEELGLGPPRPQVLA 636
Db 567 -----GLLGP RPQVLA 578

RESULT 7
US-09-692-504-1
Sequence 7, Application US/08653740
Patent No. 5792850
GENERAL INFORMATION:
APPLICANT: James W. Baumgartner
APPLICANT: Donald C. Foster
APPLICANT: Frank J. Grant
APPLICANT: Cindy A. Sprecher

TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,740
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 623 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-740-7

Query Match 58.4%; Score 2044; DB 1; Length 623;
Best Local Similarity 62.8%; Pred. No. 1.7e-160;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

14 LPKALLPLLWLFQTRPQGSAGPLQCYGVGPGDLNCSWEPLGDLGAPSELHLSQKY 73
9 LTPLELLLSLMLGTRPHGSPGLQCYGVGPGDLNCSWEPLGDLTPVLYHQSOKY 68
Qy 74 RSNKQTQVAVAGRSWVAIPREQLTMSDKLLVWGTAKAGPLPPVFNLETKMKNAPRL 133
Db 69 HFNRVHEVVPKQSWVTIPREQFTMADKLLWGTQGRPLWSSVSNLETKMKNAPRL 128
Qy 134 GPDVDFSEDDPLEATVHWAPTPWPSHKVLICOFHYRRCOEAAWTLLEPELKTPLTPVEI 193
Db 129 FSQVDISEATLEATVQWAPPVWPPKALTCQFRYKECQAEAWTRLEPQLKTDGLTPVEM 188
Qy 194 QDELEATGYKYVGRCMKEEDLWSEWSPILSFQTPPSAPKDVWVSGNLCGTPGGEEPLL 253
Db 189 QNLEPCTCYQVSRQVENGYP-WGEMSSPLSFQTPFLDPEDVWVSGTVCETSGKRAULL 247
Qy 254 LKAKGPCVQVQSYKVFVWGGRELSPEGITCCSLIPSGAEWARVAVNATSWPELTLNLS 313
Db 248 VNKDPRPCVQVYTVWFGADITTTQEEVPCCKSPVPAWMEVAVVSGNSTSWVPTNLS 307
Qy 314 LVCLDSASAPRSVAVSSVWGGRELSPEGITCCSLIPSGAEWARVAVNATSWPELTLNLS 373
Db 308 LVCLAPESAPCDVGVSSADGSPGKVTWKQGRKPLEYVVDNAQGDGSLDKLNTLRPPG 367
Qy 374 NLSALLPGNFTVGVYRITVAVSAGLSASVWGFREELAPLVGPTLWRLQDAPPGTP 433
Db 368 NLSTLLPGFEKGGVYRITVAVSAGLSAAPVWGFREELVPLAGVWVRLPDDPGTP 427
Qy 434 ATAMGEVPRHQLRGLHLYTLCAQSGTSPSVCMNYSNGTQSVTLPLDLPWGCPCLWVAST 493
Db 428 VVAMGEVPRHQLRGLHLYTLCAQSGTSPSVCMNYSNGTQSVTLPLDLPWGCPCLWVAST 487
Qy 494 IACQGGPPGPIRLHLPDNTLRKVLPGILFLWGLFLLGGLSLATSG 549
Db 488 VAGQGGPPGPIRLHLPDNTLRKVLPGILFLWGLFLLGGLSLATSG 547

Qy	14	LPKLALLPLLWVLEQRTTRPOGSACPLQCYGVGPGLDNCWEPGLDGLGAPSELHLQSQRY	73
Db	9	LTPLELLLSLMSLLGTRPHGSPCLQCYSVGPLGLTINCWEPGLDLETTPVLYHQSQRY	68
Qy	74	RSNKTOIVAVAGRSWAIPREGLTMSDKLLVWGTKAGOPLMPPVFNLETQMKNPAPRL	133
Db	69	HPNRVIEVKVPSKQSWTIPREGFTWADKLLIWGTQGRPLWSSVSNLETQMKPDTPOI	128
Qy	134	GPVDIFSEDDPLEATVHWAPPTWPSHKVLICQPHYRRQCEAAWTLLEPELKIPTLPVEI	193
Db	129	FSQVDISEEATLEATVQWAPPVPPQKALTCQFXYKECQAEATWRLPEQLKTDGLTPVEM	188
Qy	194	ODLELATGKYVGRGRMEKEEDLWGNWSPILFSQTPPSAPKQVWVYSGNLCGTPGGEPLL	253
Db	189	QNLPEGTCTQVSGRCQVENGYP-WGSEWSSPLSQTPFLDPEDWVYSGTVCETSGRAALL	247

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RESULT          9
US-09-275-925-7
; Sequence 7, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/275,925
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-275-925-7

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Query Match	58.48;	Score 2044;	DB 3;	Length 623;
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;; GENERAL INFORMATION:
;; APPLICANT: Gubler, Ulrich A
;; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hoffmann-La Roche Inc.
;; STREET: 340 Kingsland Street
;; CITY: Nutley
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 07110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/915,495
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/685,118
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Silverman, Robert A.
;; REGISTRATION NUMBER: 35,682
;; REFERENCE/DOCKET NUMBER: CD 9195
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (201) 235-2863
;; TELEFAX: (201) 235-2363
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 862 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-915-495-2

Query Match 10.9%; Score 380; DB 2; Length 862;

Best Local Similarity 25.3%; Pred. No. 6.2e-23;

Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGAGPLQCYGVGPGDLNCSWEPLGD-----LGAPSELHLQSQ----- 71
Db 126 QPQN-----LSCIQKGQGVACTWGRGTRTHLYTEYTLQSLGPKNTWQCKDIYCDYL 181
QY 72 -----KYRSNKTQTV-AVAAGRSWVAIPREQLTMSDKLLVMGCKAGQPLWPPFVN 121
Db 182 DFCINLTSPESPENFTAKVTAVNSLGSLSLP-STFTFLDIV-----RPL-PPWDIR 231
QY 122 LETQMKPNAPRLGPDVDFSEDDPLEATVHWAPPTWFSKVLICQFHYRCQEAATLLLEP 181
Db 232 IKFQ-KASVSR-----CTLWVR-----DEGLVLNRLRYRPSNRLNMN----- 269
QY 182 ELKTIPLTPV-----ETQDLELATGYVYKCRKEKEDLWGEWSPLTSFOTP---PSAPK 234
Db 270 -----VNVTKAGRHDLDLKPTTEYEFQISSKLHLKGSWDSLSRAQTPEEPTGML 325
QY 235 DVWVSNLCGTGGEPLLLWK-----APGPCVQVSYKVFWFWVGRELSPE--GITCC 286
Db 326 DVWYMKRHIDY-SROQISLFWKNLSVSEARGKILHYOVTLQELTGCKAMTONTIGHTSWT 384
QY 287 SLIPSAEWA-RVSAVNA--TSWEPLTNLSLYCLDSASAPRSVAVSYAGSTELLWTQOP 343
Db 385 TWIPRTGNNAVAVSAANSKSSLPTRINTMNICEAGLAPRQVSANS-ECMDNILVTWQP 443
QY 344 ---GQCEPLEHVVDWAR---DGDPLEKLNWRLPPGNLSALLPGNFTVGPVYRITVTAVS 397
Db 444 PRKPSAVQEVVVEWRELHPGGDTQVPLNWLRSRPNVNSALISENKSICYEIRVYALS 503
QY 398 ASGLASASSWGFREELAPLVGPTLWRLQDAPPGTPTAIWGEVPRHLRGLHLYTLCLC--- 455

Db 504 GD-QGCSILGNSKHKAPLSGPHINAITE-EKGSILISWNSIPVQEQMGCLLHYIYWK 561
QY 456 -AQSGTSPSVC---MNVSGNTQSVTLPLDLPWGCELMWVTASTIAGOGPPGPIRLRLHPDN 511
Db 562 ERDSNSQPQLCEIPYKVSQNSHPINSIQ-PRVTYVLMWTALTAAAGSSHGNEREFCL-QG 619
QY 512 TLRWK--VLPGI---LFLWGLFLLGCGLSLATSGRCYHLRHVKYL-----PRWVWEKVP 559
Db 620 KANWMAFVAPSGICAIIMVGIF-----STHYFOOKVFVLLAALRPQWCSREIP 667
QY 560 DPANSSGQPH-----MEQVPEAQPLGDLPILEVEEMEPNPPVMESSQPAQATA-----PLD 610
Db 668 DPANSTCAKKYPTAEKTLPLDLRLIDWPTPE---DPEPLVISEVLHQVTVFVRHPPC 723
QY 611 SGYEKHFLLTPPELGLLG-----PPRQVQL 635
Db 724 SNWPQ-----REKGIQGHQASEKMMHSASSPPPPRAL 756

RESULT 12

US-08-914-520-2
; Sequence 2, Application US/08914520
; Patent No. 5919903
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,520
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,118
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 862 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-914-520-2

Query Match 10.9%; Score 380; DB 2; Length 862;

Best Local Similarity 25.3%; Pred. No. 6.2e-23;

Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

QY 31 RPOGAGPLQCYGVGPGDLNCSWEPLGD-----LGAPSELHLQSQ----- 71
Db 126 QPQN-----LSCIQKGQGVACTWGRGTRTHLYTEYTLQSLGPKNTWQCKDIYCDYL 181
QY 72 -----KYRSNKTQTV-AVAAGRSWVAIPREQLTMSDKLLVMGCKAGQPLWPPFVN 121

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Db 182 DFGINTPESPNFTAKVTAVNSLGSSSLP-STFTFLDIV-----RPL-PPWDIR 231
Qy 122 LETOMKPNAPRLGPDVDESDPLATVHWAPPTWPSHKVLICQFHYRCQEAANTLLEP 181
Db 232 IKFO-KASVSR-----CTLYWR-----DEGLVLLNRLRYRPSNRLNM--- 269
Qy 182 ELKTIPLTPV---BIQDELATGKYYVGRCRMEKEEDLWGSFILSFQTP---PSAPK 234
Db 270 ----VNVTKAKGRHLLDLKPTFEFQISLKLHLYKGSWSWSLRAQTPPEEPTGML 325
Qy 235 DVWVSGNLGPTGPEEPLLMK-----APGCVQVSKYVFWVGGRELSPE---GITCCC 286
Db 326 DVWYMKRIDY-SROISLFWKNLSVSEARGKILHYQVTLQELTGKAMTQNTIGHTSWT 384
Qy 287 SLIPSGAEMA-RVSAVNA--TSWEPLTNLSLCLDSASAPRSVAVSSVSTAGSTELLVWQP 343
Db 395 TVIPRTGNWAVASANKGSLPTRINIMNLCEAGLLAPROVSANS-EGMDNILVWQP 443
Qy 344 ---GGEPELHVVDWAR---DGDPLEKLNWVRLPPGNLSALLPGNFTVGVYRITVAVS 397
Db 444 PRKDSAVQEVYVENRELHPGDDTVPLNWLRSRPNVNSALISENISKYICVEIRVIALS 503
Qy 398 ASGLASASVWCFRELAPLVPPTLWRLODAPPTGPTATANGVPRHQLRHLTHYTLG--- 455
Db 504 GD-QGCGSSILGNSHKAPLSPHINATE-EKGSILISWNSIPVQEQMGCLLHYRIYWK 561
Qy 456 -AQSGTSPSVC---MNVSGTOSVTLPLDLPWGPCBLWVTAAGGPPGPILRLHLPDN 511
Db 562 ERDSNSQOLCEIPRVSONSHINSLO-PRVYVLMWLTALTAAGSSHGNREFCLO-OG 619
Qy 512 TLRWK--VLPGI---LFLWGLFLCCGLSLATSGRCYHLRHKV-----PRWYMEKVP 559
Db 620 KANMAFAPSICIAIIMVGIF-----STHYFOQKVFVLLAALRPQWCSREIP 667
Qy 560 DPANSSGQPH-----MEQVPEAQGLDLPLEVEEMEPVWESSQPAQATA-----PLD 610
Db 668 DPANSTCAKKYPIABEKTOLPLRLDILDMPTPE-----DPEPLVISEVLHQVTPVFRHPPC 723
Qy 611 SGYKHFLLPTPEELGLG-----PPRPQVL 635
Db 724 SNWPQ-----REKIGHQHASEKDMHMSASSPPPPRAL 756

RESULT 13
5422248-2
; APPLICANT: SMITH, CRAIG A.;LARSEN, ALF D.;SIMS, JOHN E.;
; APPLICANT: CURTIS M.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING GRANULOCYTE-COLONY
; STIMULATING FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/6,183
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 587,329
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 522,952
; FILING DATE: 03-APR-1990
; APPLICATION NUMBER: 416,306
; FILING DATE: 03-OCT-1989
; APPLICATION NUMBER: 412,816
; FILING DATE: 26-SEP-1989
; SEQ ID NO.: 2
; LENGTH: 783
5422248-2
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Query Match 8.5%; Score 298.5; DB 6; Length 783;
Best Local Similarity 22.5%; Pred. No. 2.9e-16;
Matches 160; Conservative 75; Mismatches 250; Indels 227; Gaps 34;
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Qy 50 LNCMSPEPLDGLGAPSELHQSQYRSN-KTQTVAV-----AAGRSWVAIPREOLTMSDKL 103
Db 140 LICOWEPGPEETHLPTSTLKSFKSGRCNCOTQDSILDCVPKDGQSHCCIPRKHLLLYQNM 199
Qy 104 LVN-----GFKAGOPW-----PPVFVNLETOMKPNAPRLG-----PDVDF 139
Db 200 GIWQOANALGTSMSQCLDPMDDVVKLEPPMLRTMDPSPEAAPQAGCQLCWEP----- 255
Qy 140 SEDDDPLEATVHWAPPTWPSHKVLICQF-HYRCQEAANTLLEPELKTIPLTPTVEIQDEL 198
Db 256 -----WQPGHLINQK---CELRIKPKQGEASWALVGP-----LPLEALQYEL 294
Qy 199 -----ATGKYYVGRCRMEKEEDLWGSFILSFQTPPSAPK-----DVWVSGNLGCTPGGEE 250
Db 295 CGLLPATATVTLQIRCIWPLPGHWSWDSLSLELRTERRAPTVRDLTW----- 341
Qy 251 PLLLLKAPCPQVQVSKYVFWVGGRELSPEGTCCSLIPSGAEWARSVAVNATSEHP--- 308
Db 342 ---WRQ-----RQDPRTVOLFVKPVPLEEDSGRIQGY-VVSWRPSG 379
Qy 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSVSIAGST----- 335
Db 380 QAGAILPLCNTTETSLCTFHLPSAQEVALVAYNSAGTSRPTPVFSESRGPAITRLHAMA 439
Qy 336 -----ELLVTWQPCGPELHVVDWARDGDPLEKLN--WVRLPPGNLSA-LLPGNFTVGP 388
Db 440 RDPHSLWGWEPNPMWPGYVIEWGLGPPSASNSKNTWRMEQNGRATGFLKENIRPFOL 499
Qy 389 YRITVTVASASGLASASSVWGPREELAPLVGLPTLWRLODAPPTGPTATANGVPRHQLRGH 448
Db 500 YEIIIVTPLYQDTMGPSQHVYAYSOEMAPSHAPEL-HLKHIGKTAQLEWVPEPELKGSP 558
Qy 449 LTHYTLCAQSGTSPSCVMNVSGTOSVTLPLDLPWGPCBLW-----VTA 491
Db 559 LTHYTLFTWNAQNSFSAITLNASSRGFVLHGLE--PASLYHIHLMAASQAGATNSVTLT 616
Qy 492 STIAQGGPGPILRLHLPDLNTPLRKVKVLPGLIFLWGLFLL---GCGLSLATSGRCYHLRHK 548
Db 617 MTLTPEGS-----ELHI-----ILGLFGLLLLTCLCG---TAWLCCSPNRK 655
Qy 549 VLPWVWKEVDPDPANSSSG-----QPHMEQVP--EAQPLDGLPILVEEEMEP--- 595
Db 656 ---NPLWSPVDPFAHSSLSGWSVPTIMEEDAFQLPGGLGTPPTKLTVLEDEKKVPWESH 712
Qy 596 -----VMESSQPAQATAP-LDSGYEKHFLLPTPEELGLLGP 631
Db 713 NSSETCGLPTLVQTVYVLOGDPRAVSTQPOSQSG-----TSQ-----AGPPR 754

RESULT 14
US-07-923-976-4
; Sequence 4, Application US/07923976
; Patent No. 5574136
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigekazu
; APPLICANT: Fukunaga, Rikio
; TITLE OF INVENTION: DNA Encoding Granulocyte
; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones, Tullar & Cooper, P.C.
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,976
; FILING DATE: 19920922
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74539/1990
; FILING DATE: 23-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 176629/1990
; FILING DATE: 03-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP91/00375
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hellwege, James W.
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 514853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-1500
; TELEFAX: 703-415-1508
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 836 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-923-976-4

Query Match      8.5%; Score 297.5; DB 1; Length 836;
Best Local Similarity 22.8%; Pred. No. 3.8e-16;
Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;

QY 50 LNCSEPLDGLGAPSELHLQSKYRSN-KTQTVAV-----AAGRSWAIPREOLTHSDKL 103
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 140 LICQWEPGPELHPTFTLKSEKSRGNCOTQGSILDCVPKQSQHCCIPRKHLLYQNM 199
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 104 LVW-----GKAGQPLW-----PPVFVNLETKMKPNAPRLG-----PDVDF 139
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 200 GIWVQAEALGTSMSPOLCLDPMVVKLEPPMLRTWDPSPEAAPQAGCLQLCWEP--- 255
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 140 SEDDPLEATVHMAPTPWPSHKVLICQF-HYRRCQEAANTLLEPELKTPIPTVPEIQDLEL 198
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 256 -----WQGLHINQ-----CELRHKPQGEASWALVGP-----LPLEALQYEL 294
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 199 -----ATGKYVGRCRMEKEEDLWGEWSPILSQTPPPSPAK-----DWMVSGNLCGTPGGEE 250
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 295 CGLLPATAYTLQIRCIWPLPGHWSWSPSLRLTTERAPTVRLDTW----- 341
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 251 PLLLWAPGCVQVSKYKVFVWVGGRGELSPGELTCCCLIPSGAEWARSVAVNATSWEP-- 308
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 342 ----WQ-----ROLDPRTVOLFWKPVLEEDSGRIQGY-VVSWRPSG 379
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAGST----- 335
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 380 QAGAILPLCMTTSLCTFHLPSAEQVALVAYNSAGTSRPTPVFSESRGPAITRLHAMA 439
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 336 -----ELLVTWQPGPGPLEHVVDWARDGPLEKLN--WYRLPPGNLSA--LLPGNFTVGVVP 388
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 440 RDPHSLWVGWEPNPWPGVYVIEWGLGPPSASNSNKTWRMEQNGRATGFLKENIRPFQL 499
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 389 YRITVTAVSASGLASASSVWGRPREELAPLVGPTLWLQDAPPCTPAIANCEVPRHQLRGH 448
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 500 YEIVTPLYQDTPGSHVAYSCWEMAPSHAPEL-HLKHIGKTWAEQLEWVPEPELGKSP 558
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 449 LTHYTLCAQSGTSPSCVMNVSGMTQSVTLTDLPLWPGPCELW-----VTA 491
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 559 LTHYTIFTWNAQNSQSFALINASSRGFVLHGLE--PASLYHITHLMAASQAGATNSVLT 616
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 492 STIAGGPGPGPIRLHLDPNTLRNWKVLPGLILFWGLFLL---GCGLSLATSGRCYHLRHK 548
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 617 WTLTPRGS-----ELHI-----ILGLFGLULLLTCLCG---TAWLCCSPNRK 655
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 549 VLPWRWKEKVPDPANSSG-----OPHMEQVP--EAOPLGDLPLILEVEEMEPVPMES 599
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 656 ---NPLWSPDPFAHSSLSGWSVPTIMEEDAFQLPGLGLTPTTKLTIVLEEDKKVPV-WES 711
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
```

```

QY 600 SOPAQATAPLDSCYEKHFLEPTPEELGILL-GPPR 631
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 712 HNSSETCG-----LPTLVQTVVLQGDPR 734
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 15
US-08-419-652-6
; Sequence 6, Application US/08419652
; Patent No. 5831007
; GENERAL INFORMATION:
; APPLICANT: Chua, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,652
; FILING DATE: 11-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,532
; FILING DATE: 31-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/094,713
; FILING DATE: 19-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: CD 9174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..602
; OTHER INFORMATION: /note= "Represents residues 98 to
; OTHER INFORMATION: 731 of human granulocyte colony-stimulating
; OTHER INFORMATION: factor-receptor."
; US-08-419-652-6

Query Match      8.4%; Score 294.5; DB 2; Length 602;
Best Local Similarity 22.7%; Pred. No. 4.2e-16;
Matches 149; Conservative 70; Mismatches 240; Indels 197; Gaps 30;

QY 50 LNCSEPLDGLGAPSELHLQSKYRSN-KTQTVAV-----AAGRSWAIPREOLTHSDKL 103
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 21 LICQWEPGPELHPTFTLKSEKSRGNCOTQGSILDCVPKQSQHCCIPRKHLLYQNM 80
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 104 LVW-----GKAGQPLW-----PPVFVNLETKMKPNAPRLG-----PDVDF 139
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 81 GIWVQAEALGTSMSPOLCLDPMVVKLEPPMLRTWDPSPEAAPQAGCLQLCWEP--- 136
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 140 SEDDPLEATVHMAPTPWPSHKVLICQF-HYRRCQEAANTLLEPELKTPIPTVPEIQDLEL 198
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
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Db 137 -----WOPGLHINQK---CELRRHKPORGEASNALVGP-----LPLEALQYEL 175
Qy 199 -----ATGYKYVGRCKMEKEEDLWGEWSPILSFQTPPSAPK---DVWYSGNLCTPGGEE 250
Db 176 CGLLPATAYTLQIRIRWPLPGHWSWSPSLERLRTTERAPTVRDLTW----- 222
Qy 251 PLLLWKAPGPCVQVSYKWFVWGGRELSPEGITCCCSLIPSGAEWARVSANVATSWEP-- 308
Db 223 ----WRQ-----RQDPRTVQLEWKPVPLEEDSGRIQGY-VVSWRPSG 260
Qy 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSITAGST----- 335
Db 261 QAGAILPLCNTTELCTHLPSEAOEVALVAYNSAGTSRPTVPVFESESGPALTRLHAMA 320
Qy 336 ----ELLVTWQPGGEPLEHVVDWARDGDPLEKLN--WVRLPPGNLSA--LLPGNETVGVY 388
Db 321 RDPHSLWGWEPNPWPQGYVEMCLGPPSASNSNKTWRMEQNGRATGFLLENIRPEQL 380
Qy 389 YRITVTAVSASGLASASSWGFREELAPLVGPTLWRLQDAPGTPAIANGEVPRHQLRGH 448
Db 381 YEIIIVPLYQDTMGPSQHVYAYSQEMAPSHAPEL-HLKHIGKTAQLEWVPEPPELGKSP 439
Qy 449 LTHYTLCAQSGTSPSVCMNVSGNTQSVTLPLDPWGPCELW-----VTA 491
Db 440 LTHYTFWTNAQNGSFSAILWASSRGFVLHGLE--PASLIHILHMAASQAGATNSTVLT 497
Qy 492 STIAQQGPPGPIRLHLPDNTLRWKVLPGLFLWGLFLL--GCGLSLATSGRCYHLRHK 548
Db 498 MTLTPEGS-----ELHI-----ILGLFGLLLLTCLCG-----TAWLCCSPNRK 536
Qy 549 VLPWRVWEKVPDPANSSG-----QPHMEQVP--EAQPLGDLPILEVEEMEPP 595
Db 537 ---NPLWPSVPDPAHSSLGSWVPTIMEEDAFQLPGLGTPPTITKLVLEDEKKVP 589

Search completed: May 9, 2002, 06:04:24
Job time: 36 sec

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GenCore version 4.5
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OM protein - protein search; using sw model

Run on: May 9, 2002, 06:05:05 ; Search time 30.82 Seconds
(without alignments)
1539.804 Million cell updates/sec

Title: US-09-692-504-2
Perfect score: 3424
Sequence: 1 MNRRLVARLTPLLELLSLMS.....IVSGYKHFLLPTPEELGLLV 623
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2044	59.7	636	2 JW0047	class I cytokinase
2	277	8.1	1097	2 S17308	leukemia inhibitor
3	270	7.9	918	2 A36337	membrane glycoprot
4	261	7.6	783	2 JH0329	granulocyte colony
5	255.5	7.5	837	2 A34898	granulocyte colony
6	253	7.4	863	2 C38252	granulocyte colony
7	252	7.4	1092	2 JX0312	differentiation-st
8	244	7.1	917	2 I49699	glycoprotein 130
9	228	6.7	771	2 B38252	granulocyte colony
10	223	6.5	918	2 A44257	interleukin-6 sign
11	165.5	4.8	581	2 I45971	prolactin receptor
12	163	4.8	622	2 A40144	prolactin receptor
13	163	4.8	1259	2 A43425	Bravo/Nr-CAM cell
14	161	4.7	878	1 A40091	interleukin-3 rece
15	161	4.7	26926	1 I38344	titin, cardiac mus
16	160.5	4.7	1825	2 T32828	hypothetical prote
17	158	4.6	1268	1 A39640	neural cell adhesi
18	154	4.5	895	2 S74225	leptin receptor, i
19	153	4.5	892	2 S68439	leptin receptor, s
20	153	4.5	894	2 S88437	leptin receptor, s
21	153	4.5	900	2 S68440	leptin receptor, s
22	153	4.5	1162	2 S68438	leptin receptor, s
23	153	4.5	1197	2 T30581	neural cell adhesi
24	151.5	4.4	2944	2 A54849	collagen alpha 1(V
25	151	4.4	1344	2 T14316	rig-1 protein - mo
26	148	4.3	1162	2 PC4184	leptin receptor, O
27	148	4.3	2477	2 S14428	fibronectin precu
28	146	4.3	13055	2 T16580	hypothetical prote
29	145	4.2	2029	1 TDFFLK	protein-tyrosine-p

30 144.5 4.2 2302 2 T14328 protein-tyrosine-p
31 143.5 4.2 310 2 A29884 prolactin receptor
32 142.5 4.2 412 2 A41070 prolactin receptor
33 142.5 4.2 610 2 A34631 lactogen receptor
34 142.5 4.2 610 2 A36116 prolactin receptor
35 142.5 4.2 1028 2 A53449 plasmacytoma-assoc
36 142 4.1 2481 2 A43908 fibronectin - Airi
37 141 4.1 805 2 S68441 leptin receptor, s
38 141 4.1 1914 2 T42635 tenascin Y precurs
39 140.5 4.1 616 2 A30304 prolactin receptor
40 140.5 4.1 1711 1 A55148 protein-tyrosine-p
41 140.5 4.1 1896 2 T08851 Down syndrome cell
42 139.5 4.1 292 2 I77525 prolactin receptor
43 139.5 4.1 303 2 I77524 prolactin receptor
44 139.5 4.1 608 2 I53269 prolactin receptor
45 138.5 4.0 635 2 A45266 MPL-P protein prec

ALIGNMENTS

RESULT 1
JW0047
class I cytokinase receptor precursor - human
N:Alternate names: WSX-1
C:Species: Homo sapiens (man)
C:Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000
C:Accession: JW0047
R:Spiecher, C.A.; Grant, F.J.; Baumgartner, J.W.; Presnell, S.R.; Schrader, S.K.; Yam
Biochem. Biophys. Res. Commun. 246, 82-90, 1998
A:Title: Cloning and characterization of a novel class I cytokine receptor.
A:Reference number: JW0047; MUID:98262921
A:Accession: JW0047
A:Molecule type: mRNA
A:Residues: 1-836 <SPR>
A:Cross-references: GB:AF053004; NID:g3153240; PIDN:AAC39755.1; PID:g3153241
A:Experimental source: brain
C:Genetics:
A:Map position: 19p13.11
C:Keywords: glycoprotein
F:1-32/Domain: signal sequence #status predicted <SIG>
F:515-540/Domain: transmembrane #status predicted <TMM>
F:554-561/Domain: cytoplasmic #status predicted <CTP>
F:51.76.302.311.374.382.467/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 59.7%; Score 2044; DB 2; Length 636;
Best Local Similarity 62.8%; Pred. No. 2.2e-133;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;
QY 9 LTPLELLSLMLLLGTRPHGSPGLQCYSGVPLGTLNCSWEPLGDLETPPVLYHQSKY 68
DB 14 LPKALLPLLVLFORTPQGSAGPLQCYGVGPLGDLNCSWEPLGDLAGPSELHQSKY 73
QY 69 HPNRVWEKVPKSPQWVTTPREQFTMAKLLIWTGKGRPLWSSVSNLETQKPDTPQ 128
DB 74 RSNKQTAVAGRSWVAIPQLTMSDKLLVWGKAGOPLPWPVFNLETOMKNAPRL 133
QY 129 FSQVDISEATLEATVQWAPPVWPQKALTCQFRYKECAEAWTRLEPOLKTDGLTPVEM 188
DB 134 GPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCOEAAWTLLEPELKIPLTPVEI 193
QY 189 QNLEPCTCQVSGRCQVENGYP-WGEWSSPLSFQTPFLDPEDVWVSGTVCETSGRAALL 247
DB 194 QDELATGKVVYGRCKMEEDLNGEWSPLSFQTPPSAPKDVWVSGNLCGTPGGEEL 253
QY 248 VNKDRPCQVQTYTVFAGDITTTQEEVPCCKSPVAMWNAWVSPGNSTSWVPPTNLS 307
DB 254 LMKAGPCVQVQYKVFVWVGGRLESPGEGTCCCSLIPSAEAWARVSNATSWEP 313
QY 308 LVCLAPESAPCDGVSSADSGSPIKVTKQGRKPLLEYVYVDAQDGLSKLNTWRLPPG 367
DB 314 LVCLDSASAPRSVAVSSITAGSTELLVTVWGPGEPLHVVDWARDGDPLKLNWRLPPG 373

Result No.	Query			ID	Description
	Score	Match	Length		
1	384	11.2	862	1 I12S_HUMAN	Q95665 homo sapien
2	339.5	9.9	874	1 I12S_MOUSE	P97378 mus musculus
3	277	8.1	1097	1 L1FR_HUMAN	P42702 homo sapien
4	270	7.9	918	1 I16B_HUMAN	P40189 homo sapien
5	261	7.6	836	1 GCSR_HUMAN	Q95062 homo sapien
6	255.5	7.5	837	1 GCSR_MOUSE	P40223 mus musculus
7	252	7.4	1092	1 L1FR_MOUSE	P42703 mus musculus
8	244	7.1	917	1 I16B_MOUSE	Q00560 mus musculus
9	223	6.5	918	1 I16B_RAT	P40190 rattus norv
10	177.5	5.2	581	1 PRUR_CEREL	Q28235 cervus elap
11	165.5	4.8	581	1 PRUR_BOVIN	Q28172 bos taurus
12	163	4.8	622	1 PRUR_HUMAN	P16471 homo sapien
13	158	4.6	1284	1 NRCA_CHICK	P35331 gallus gall
14	157	4.6	878	1 I13B_MOUSE	P28954 mus musculus
15	154	4.5	639	1 CAIC_RABIT	Q28902 oryctolagus
16	153	4.5	1162	1 LEPR_MOUSE	P48356 mus musculus
17	151.5	4.4	2944	1 CA17_HUMAN	Q02388 homo sapien
18	148	4.3	1162	1 LEPR_RAT	Q62959 rattus norv
19	148	4.3	2477	1 F1NC_RAT	P04937 rattus norv
20	145	4.2	2029	1 LAR_DROME	P15621 drosophila
21	142.5	4.2	610	1 PRUR_RAT	P05710 rattus norv
22	142.5	4.2	1711	1 PTPO_RAT	Q64612 rattus norv
23	142	4.1	1705	1 PTPO_MOUSE	P70289 mus musculus
24	142	4.1	3067	1 CAIC_MOUSE	Q60847 mus musculus
25	140.5	4.1	616	1 PRUR_RABIT	P14787 oryctolagus
26	140.5	4.1	2012	1 DSCA_HUMAN	Q60469 homo sapien
27	140.5	4.1	3063	1 CAIC_HUMAN	Q93715 homo sapien
28	139.5	4.1	608	1 PRUR_MOUSE	Q08501 mus musculus
29	138.5	4.0	635	1 TPOR_HUMAN	P40238 homo sapien
30	138.5	4.0	896	1 CYRB_MOUSE	P28955 mus musculus
31	138	4.0	897	1 CYRB_HUMAN	P32927 homo sapien
32	138	4.0	1493	1 NEOL_MOUSE	P97798 mus musculus
33	137	4.0	2481	1 F1NC_XENIA	Q91740 xenopus lae

FT DOMAIN 519 607 FIBRONECTIN TYPE-III 3.
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 862 AA; 97134 MW; 67COE0D946B8DD58 CRC64;

Query Match 11.2%; Score 384; DB 1; Length 862;
 Best Local Similarity 25.1%; Pred. No. 8,1e-21;
 Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;

QY 5 RVARLTPELLLSMLSLGTRPHSGPGLQCYSGVPLGLTNCWEPGLD--LETTPVLY 62
 Db 102 KLACINSDEIQICGAEIFGVAF-EQNLSCIQKEGGQVACTWGRGRTHLYETTLQ 160
 QY 63 HQSQKYHPRNVK-----VPSKQSWVTPREQFTWADKLLIWGTQGR 107
 Db 161 LSGPK---NLTWQKCKDYCDYLDGFINLTPES-----PESNFAKVTAV-----N 204
 QY 108 PLWSSVSVNLETKMPTDPOIFSQVDISEATLEATVQWAPPVWPP-----OKA----- 156
 Db 205 SLGSSSL-----PSTFTFLDI-----VRPLPP-WDIRKFKQASVRSCTL 244
 QY 157 -----LTCQFRYKCOAEATRLPOLKTDGLTPVEMONLEPTCY--QVSGRCQVE 206
 Db 245 YWRDEGLVLLNRLYRPSNLSLNMWYN---VTKAGRHLDLDDKPTTEYEFQISSKLHY 301
 QY 207 NGYGEWSSPLSFQTFPDLPE---DWVSGTVCTSGKRAALLVWK-----DPRPCV-- 256
 Db 302 KG-SWSDSSSLAQTPPEEPTGMDVWYMKRHIDYSRQOISLF-WKNLSVSEARGKILH 359
 QY 257 -QVTVVWFAGADITTOEVEVPCCKSPVPAWMEVAV-VSPGNSTSVVPTNLSL--VCLA 312
 Db 360 YQVTLQELTGGKAMTQITGHTSWTTPVIRPTGNWAVAVSAANSKSSLPTRINIMNLCEA 419
 QY 313 PESAPCDVGVSSADGSPGIKVTWKQTRKP---LEVVDWAQ---DGDSDKLNWTRLPP 366
 Db 420 GLLAPQVANS-EGMDNLLVWQPRKDPQSAVQEVVREWLHPGQDQVPLNWLRSRP 478
 QY 367 GNLSTLLPGCFKGVPIRTVAVYSGGLAAPSVMGFEELVPLAGPAVWRPLDPPPT 426
 Db 479 YNVSALISENIKSYICVIRVYAL-SGDQGCSSILGNSKHKAPLSGPHINAITEB-KGS 536
 QY 427 PVYAGVPRHQLRGQATHYTFIQSRGLSTVCRNVSSQTQTATLP-----NLH----- 475
 Db 537 ILISWNSIPVQEQMGLLHYRYWKE-----RDSNSQPLCEIPYRVSQNSHPINSLQ 589
 QY 476 -SGSFLKWTVTSVVAGOGPGPDLHLDPNRLRWKALPFLSLWGLLGMCGLSLASTR 534
 Db 590 PRVTVVLMWLTAAESSHGNRECL-QGKANWMAFVAPSICIAIIVG-----TFSTH 644
 QY 535 CLQARCLHWRHKLHPQWIERVDPDANSNGQPY-IKEYSLQP-----PKDGPI 593
 Db 645 YFOQVFLVLAALRPQWCSREIPDPANSTCAKKYPYIAEETQLPLDLLIDWPTPEDPEP 704
 QY 584 LEVEEV--ELQPVESPAS 601
 Db 705 LVISEVLHQTVPVFRHPPCS 724

RESULT 2

ID I125_MOUSE STANDARD; PRT; 874 AA.
 AC P97378;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-

DE 2) (IL-12R-BETA2).
 GN IL12RB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RP [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97098510; PubMed=8943050;
 RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
 RA Gately M.K., Gubler U.;
 RT "A functional interleukin 12 receptor complex is composed of two
 RT beta-type cytokine receptor subunits.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
 CC -!- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
 CC LOW AFFINITY.
 CC -!- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
 CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
 CC IL12RB2.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC -----
 CC EMBL; U04199; AAB36676.1; -;
 DR HSSP; P40189; 1BQJ.
 DR MGD; MGI:1270861; IL12RB2.
 DR InterPro; IPR002996; CRJA.
 DR InterPro; IPR001777; FN.III.
 DR InterPro; IPR003549; Hematopo_rceptor_L_F2.
 DR Pfam; PF00041; fn3; 4.
 DR PRINTS; PRO0014; FNTYPEIII.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 KW SIGNAL 1 20
 FT CHAIN 21 874
 FT OR 23 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT TRANSMEM 640 656
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 657 874
 FT FIBRONECTIN TYPE-III 1.
 FT DOMAIN 137 230
 FT FIBRONECTIN TYPE-III 2.
 FT DOMAIN 240 322
 FT FIBRONECTIN TYPE-III 3.
 FT DOMAIN 436 523
 FT FIBRONECTIN TYPE-III 4.
 FT CARBOHYD 48 48
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 224 224
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 252 252
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 279 279
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 323 323
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 874 AA; 98196 MW; 582E4D21BF1FBD67 CRC64;

Query Match 9.9%; Score 339.5; DB 1; Length 874;
 Best Local Similarity 22.1%; Pred. No. 1.6e-17;
 Matches 155; Conservative 108; Mismatches 279; Indels 159; Gaps 36;
 QY 19 MSLLLTTRPHSGMPGLQCYSGVPLGLTNCWEPGLDLETTPVLYHQSKYHPRNVK 78

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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:10:49 ; Search time 50.89 Seconds
(without alignments)
1790.679 Million cell updates/sec

Title: US-09-692-504-2
Perfect score: 3424
Sequence: 1 MNRRLVARLTPELLLSLMS.....IYSGYKHFLLPTPEELGLIV 623

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3424	100.0	623	11 070394	O70394 mus musculus
2	2044	59.7	636	4 O60624	O60624 homo sapien
3	345	10.1	861	6 Q9BEG2	Q9BEG2 bos taurus
4	282	8.2	971	11 070458	070458 mus musculus
5	279.5	8.2	970	11 088821	088821 mus musculus
6	278	8.1	881	13 057519	057519 xenopus lae
7	277	8.1	710	13 057520	057520 xenopus lae
8	259	7.6	1093	11 070535	070535 rattus norv
9	243.5	7.1	918	13 09W609	09W609 gallus gall
10	193.5	5.7	979	4 Q96650	Q96650 homo sapien
11	167.5	4.9	581	6 O46561	O46561 ovis aries
12	165.5	4.8	296	6 O18880	O18880 bos taurus
13	164	4.8	1140	4 Q9P218	Q9P218 homo sapien
14	163	4.8	1207	4 Q9BQ07	Q9BQ07 homo sapien
15	161.5	4.7	622	6 Q9N0J7	Q9N0J7 callithrix
16	161	4.7	26926	4 Q10466	Q10466 homo sapien
17	160.5	4.7	4280	5 Q9UB29	Q9UB29 caenorhabdi
18	160.5	4.7	4450	5 Q9UB28	Q9UB28 caenorhabdi
19	159	4.6	2944	11 O63870	O63870 mus musculus

20	156.5	4.6	1180	4 O15051	O15051 homo sapien
21	155	4.5	2016	5 Q9V4J9	Q9V4J9 drosophila
22	155	4.5	2016	5 Q9NBA1	Q9NBA1 drosophila
23	154.5	4.5	1236	4 Q9UHI3	Q9UHI3 homo sapien
24	154.5	4.5	1308	4 Q9UHI4	Q9UHI4 homo sapien
25	154	4.5	895	11 Q62960	Q62960 rattus norv
26	154	4.5	1162	11 Q9QW63	Q9QW63 mus musculus
27	153.5	4.5	1154	11 Q9QVW3	Q9QVW3 rattus norv
28	153	4.5	1147	13 Q9DDK1	Q9DDK1 meleagris g
29	153	4.5	1197	13 Q90478	Q90478 brachydanio
30	153	4.5	1299	4 O15179	O15179 homo sapien
31	152.5	4.5	1299	4 Q92823	Q92823 homo sapien
32	152	4.4	349	4 Q9UHJ5	Q9UHJ5 homo sapien
33	151	4.4	1344	11 Q9Z214	Q9Z214 mus musculus
34	149	4.4	625	6 Q9XS92	Q9XS92 trichosurus
35	147.5	4.3	920	4 Q9P232	Q9P232 homo sapien
36	146.5	4.3	1166	11 Q9QVW4	Q9QVW4 rattus norv
37	146.5	4.3	1215	11 P97686	P97686 rattus norv
38	146	4.3	13055	5 Q9N165	Q9N165 caenorhabdi
39	145	4.2	1705	11 Q9ERK5	Q9ERK5 mus musculus
40	145	4.2	2037	5 Q9VIS8	Q9VIS8 drosophila
41	144.5	4.2	2302	11 088488	088488 rattus norv
42	142.5	4.2	1028	11 Q07409	Q07409 mus musculus
43	141	4.1	1914	13 Q91008	Q91008 gallus gall
44	139.5	4.1	608	11 Q99J21	Q99J21 mus musculus
45	139.5	4.1	2013	11 Q9ERC8	Q9ERC8 mus musculus

ALIGNMENTS

RESULT 1
O70394
ID O70394 PRELIMINARY; PRT; 623 AA.
AC O70394;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR.
GN WSX1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98262921; PubMed=9600072;
RA Sprecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,
RA Schrader S.K., Yamagiwa T., Whitmore T.E., O'Hara P.J., Foster D.F.;
RT "Cloning and characterization of a novel class I cytokine receptor.";
RL Biochem. Biophys. Res. Commun. 246:82-90(1998).
DR EMBL; AF053005; AAC40121.1;
DR MGD; MGI:1355318; Wsx1.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 623 AA; 68998 MW; 4BA20FEC875A7180 CRC64;

Query Match 100.0%; Score 3424; DB 11; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.3e-261;
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNRRLVARLTPELLLSLMSLLGTRPHGSPGLOCYSGVPLGILNCSEPLGDLTPPV	60
Db	1	MNRRLVARLTPELLLSLMSLLGTRPHGSPGLOCYSGVPLGILNCSEPLGDLTPPV	60
Qy	61	LYHQSKYHPNRVWEVKVPSKQSWVTIPREQFTMDKLLIWGTQGRPLWSSVSVNLEQ	120
Db	61	LYHQSKYHPNRVWEVKVPSKQSWVTIPREQFTMDKLLIWGTQGRPLWSSVSVNLEQ	120
Qy	121	MKPDPPTQIFSQVDISEATLEATVQWAPPWPQKALTCQFRYKECOAEAWTRLEPQKLT	180
Db	121	MKPDPPTQIFSQVDISEATLEATVQWAPPWPQKALTCQFRYKECOAEAWTRLEPQKLT	180

```
Db 121 MKPDTQIFSDVISEATLEATVQWAPPVWPQKALTCQFRYKCEQAEAWTRLEPQLKT 180
QY 181 DGLTPVMQNLPGCTCYQVSGRCQVNGYPWGEWSSPLSFQTPFLDPEDVWVSGTCVETS 240
Db 181 DGLTPVMQNLPGCTCYQVSGRCQVNGYPWGEWSSPLSFQTPFLDPEDVWVSGTCVETS 240
QY 241 GKRAALLVWKDPRPCVQVYTYVWFAGDITTTQEEVPCCKSPVPANWNAVSPGNSTSW 300
Db 241 GKRAALLVWKDPRPCVQVYTYVWFAGDITTTQEEVPCCKSPVPANWNAVSPGNSTSW 300
QY 301 VPTNLNLVCLAPESAPCDGVSSADGSPGKIVTWKQGRKPLLEYVYDRAQDGLSLDKLN 360
Db 301 VPTNLNLVCLAPESAPCDGVSSADGSPGKIVTWKQGRKPLLEYVYDRAQDGLSLDKLN 360
QY 361 WTRLPNGLSTLLPGFEGKGVPRITVAVYSGGLAAAPSVWGFREELVPLAGPAWRPLP 420
Db 361 WTRLPNGLSTLLPGFEGKGVPRITVAVYSGGLAAAPSVWGFREELVPLAGPAWRPLP 420
QY 421 DDPGPTPVVAMGEVPRHQLRGQATHYTFCTQSRGLSTVCRNVSSQTQTATLPLNLHSGSEK 480
Db 421 DDPGPTPVVAMGEVPRHQLRGQATHYTFCTQSRGLSTVCRNVSSQTQTATLPLNLHSGSEK 480
QY 481 LWVTSTVAGOGPPGDLHLPLDNRIRKALPWFUSLWGLLMLGCGLSLASTRCLQARC 540
Db 481 LWVTSTVAGOGPPGDLHLPLDNRIRKALPWFUSLWGLLMLGCGLSLASTRCLQARC 540
QY 541 LHWRRHLLPQWIWERYVDPANSSGOPYIKEYSLPQPKDGPITLVEEVELOPVVESPKA 600
Db 541 LHWRRHLLPQWIWERYVDPANSSGOPYIKEYSLPQPKDGPITLVEEVELOPVVESPKA 600
QY 601 SAPIYSGYKHFLLPTPEELGLLV 623
Db 601 SAPIYSGYKHFLLPTPEELGLLV 623

RESULT 2
O60624 PRELIMINARY; PRT; 636 AA.
AC O60624;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CLASS I CYTOKINE RECEPTOR (CRLI PROTEIN).
GN WSX1 OR CRLI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OY NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:98262921; PubMed=9600072;
RA Sprechter C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,
RA Schrader S.K., Yamagata T., Whitmore T.E., O'Hara P.J., Foster D.F.;
RT "Cloning and characterization of a novel class I cytokine receptor.";
RL Biochem. Biophys. Res. Commun. 246:82-90(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., He L., Yuan Z., Cao X.;
RT "A novel glp130-like cytokine receptor.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053004; AAC39755.1; -.
DR EMBL; AF106912; AAG26090.1; -.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 636 AA; 69473 MW; DC7DAAAABA643CE97 CRC64;
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Query Match 59.7%; Score 2044; DB 4; Length 636;
Best Local Similarity 62.8%; Pred. No. 7e-153;
Matches 398; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

9 LTPLELLLSLMSLLLTGRPHSGNPLQCYSGVGLTILNCSWEPLDTPPVLYHQSQKY 68

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Db 14 LPKALLPLLWLWLFQTRPGSAGPLQCYGVPLGLDNCWEPGLDGLGAPSELHLSQKY 73
QY 69 HPNRYWEVKVPKQSWVTIPRQFTMADKLLLTWGTQKGRPLASSVSNLETKMKPDTPOI 128
Db 74 RNKQGTVAAGRSWALPREQLTMSDKLLVWGTAGQPLWPPVFNLETKMKPNAPRL 133
QY 129 FSOVDISEATLEATVQWAPPVWPQKALTCQFRYKCEQAEAWTRLEPQLKDTGLTPVEM 188
Db 134 GPVDVDFSEDDPLEATVHMAPPWPSHKVLICQHYRRCCQEAATWLTLEBELKTIPLTPEI 193
QY 189 QNLEPQTCVQSGRCOVENGYP-WGEWSSPLSFQTPFLDPEDVWVSGTCVETSGKRAALL 247
Db 194 QDLLEATGKVKYGRCRMEKEEDLWGEWSPILSFQTPPSAPKDVWVSGNLCGTPGGEPL 253
QY 248 VNKDPRPCVQVYTYVWFAGDITTTQEEVPCCKSPVPANWNAVSPGNSTSWPPTNLS 307
Db 254 LNKAPGCVQVSYKWWFWVGGRELSPEGITCCSLIPSGAEWARVSAVWATSWEPITNLS 313
QY 308 LVCLAPESAPCDGVSSADGSPGKIVTWKQGRKPLLEYVYDRAQDGLSLDKLNMTRLP 367
Db 314 LVCLDSASAPRSVAVSSVAGSTELLVWQPGCEPLEHVVDWARDGDLKLNWVRLPPG 373
QY 368 NLSTLLPGFEKGVPRITVAVYSGGLAAAPSVWGFREELVPLAGPAWRPLDPPGTP 427
Db 374 NLSALLPGNFTVGPYRITVAVSASGLASASSVWGFREELAPLVGPTLWRLODAPPGTP 433
QY 428 VVAMGVPVRHQLRGQATHYTFCTQSRGLSTVCRNVSSQTQTATLPLNLHSGSFKLWTVST 487
Db 434 ATAMGEVPRHQLRGHTHTLCAQSGTSPSCMNVSGNTQSVTLPLDPLWGPCELWATST 493
QY 488 VAGQGGPGLSLHLPLDNRIRKALPWFUSLWGLLMLGCGLSLASTRCLQARCLHWRHKL 547
Db 494 IAGQGGPGLILHLPLDNTLRNKLPLGLLWGLFLGLGGLSLATS---GRCYHLRHKV 549
QY 548 LPQWIWERYVDPANSSGOPYIKEYSLPQPKDGPITLVEEVELOPVVES---PKASAPI 604
Db 550 LPRWWEKYVDPANSSGOPYHMEQVPEAQPLGLDPLILEEVEEPPVPMESSQPAQATPL 609
QY 605 YSGYKHFLLPTPEELGLL 622
Db 610 DSGYKHFLLPTPEELGLL 627

RESULT 3
Q9BEG2 PRELIMINARY; PRT; 861 AA.
AC Q9BEG2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE IL-12 RECEPTOR BETA2 PRECURSOR.
GN IL-12R BETA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OY NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH NODE;
RA Waldbogel A.S., Zakher A., Heussler V.T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ308426; CAC28320.1; -.
KW Signal; Receptor.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 861 IL-12 RECEPTOR BETA2.
SQ SEQUENCE 861 AA; 96208 MW; 4B7B1E5D1E358E5B CRC64;
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Query Match 10.1%; Score 345; DB 6; Length 861;
Best Local Similarity 23.7%; Pred. No. 7.4e-19;
Matches 159; Conservative 110; Mismatches 297; Indels 106; Gaps 35;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2002, 06:06:12 ; Search time 43.01 Seconds
(without alignments)
1072.952 Million cell updates/sec

Title: US-09-692-504-2

Perfect score: 3424

Sequence: 1 MNKLRVARLTPELLLSLMS.....IYGVKFKFLPTPEELGLLV 623

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_ll01:*
1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT:*
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6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT:*
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14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT:*
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19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3424	100.0	623	19 AAW33400	Mouse haematopoiet
2	3424	100.0	623	22 AAU01854	Mouse type I cytok
3	2044	59.7	636	19 AAW33399	Alternatively spli
4	2044	59.7	636	22 AAU01853	Human type I cyto
5	2036	59.5	636	20 AAY29781	Human DNAX cytokin
6	1866.5	54.5	578	19 AAW33398	Human haematopoiet
7	1720	50.2	523	20 AAY29785	Partial human DNAX
8	1342	39.2	246	20 AAY29786	Partial mouse DNAX
9	712	20.8	150	20 AAY29782	Mouse DNAX cytokin
10	384	11.2	862	18 AAU2771	Human interleukin-
11	280	8.2	1001	13 AAR25068	hLIF-R, Homo sapi

12	277	8.1	1097	15	AAR49508	Human LIF-R. Homo
13	277	8.1	1097	15	AAR45776	Human leukaemia in
14	277	8.1	1097	16	AAR74097	Human leukaemia in
15	276	8.1	1001	15	AAR45774	Human leukaemia in
16	275	8.0	1001	14	AAR37806	Human LIF-R N-term
17	272	7.9	1001	16	AAR74095	Human leukaemia in
18	270	7.9	708	17	AAR85911	gp130 N-terminal f
19	270	7.9	918	12	AAR10545	Recombinant human
20	270	7.9	918	15	AAR46233	Granulocyte colony
21	270	7.9	918	21	AAY44694	Human placental G-
22	269	7.9	1001	15	AAR49506	Human granulocyte
23	264	7.7	918	17	AAR75368	Human LIF-R clone
24	261	7.6	708	14	AAR37804	Human gp130 protei
25	261	7.6	783	12	AAR11741	Human gp130 N-term
26	261	7.6	783	16	AAR77868	Granulocyte colony
27	261	7.6	783	18	AAW10485	Human placental G-
28	261	7.6	800	18	AAW10486	Human granulocyte
29	261	7.6	801	12	AAR11742	Clone 25-1 encoded
30	261	7.6	813	21	AAAB03873	Human granulocyte
31	260	7.6	836	12	AAR14255	Human GCSF recepto
32	259.5	7.6	837	12	AAR14254	Murine GCSF recept
33	253.5	7.4	1522	16	AAR70125	LIF-R-GSP 130 fusi
34	252	7.4	863	12	AAR14257	Human GCSF recepto
35	247	7.2	662	22	AAAS1244	Human haemopoietin
36	246.5	7.2	873	22	AAU02905	Angiotensin conver
37	244	7.1	652	22	AAAS1242	Human haemopoietin
38	244	7.1	917	13	AAR36334	gp130. Mus muscul
39	244	7.1	917	21	AAY55073	Mouse gp130 protei
40	232.5	6.8	775	22	AAU02904	Angiotensin conver
41	228	6.7	824	22	AAAM3678	Human EST encoded
42	227	6.6	771	12	AAR14256	Human GCSF recepto
43	226	6.6	658	17	AAR94576	Human gp130 splice
44	224.5	6.6	727	21	AAY92192	Human gp130-kappa
45	224.5	6.6	738	21	AAY92194	Human gp130-J-kapp

ALIGNMENTS

RESULT 1
AAW33400
ID AAW33400 standard; Protein: 623 AA.
AC AAW33400;
DT 22-MAY-1998 (first entry)
DE Mouse haematopoietic cytokine receptor Zcytor1.
DE Mouse haematopoietic cytokine receptor; Zcytor1; ligand detection;
KW cancer diagnosis; agonist; antagonist; murine.
OS Mus sp.
PN WO9744455-A1.
XX
PD 27-NOV-1997.
XX
PF 19-MAY-1997; 97WO-US08502.
XX
PR 23-MAY-1996; 96US-0653740.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
XX
DR WPI; 1998-018509/02.
XX
PT N-PSDB; AAT94121.
XX
PT Haematopoietic cytokine receptor - useful for ligand detection, and
XX pathological condition diagnosis
PS Claim 3; Pages 54-58; 86pp; English.

XX	CC	The present sequence is the mouse haematopoietic cytokine	
CC	CC	receptor Zcytor1, useful for ligand detection, and pathological	
CC	CC	condition diagnosis, including cancer. Receptor agonists of the	
CC	CC	protein can be used to stimulate the proliferation and development	
CC	CC	of target cells in vitro and in vivo. The agonists can stimulate	
CC	CC	cell mediated immunity and lymphocyte proliferation, to treat	
CC	CC	infection involving immunosuppression, e.g. viral infections. They	
CC	CC	may also be used to suppress tumours, induce cytotoxicity, treat	
CC	CC	leukopenias and enhance the regeneration of the T-cell repertoire	
CC	CC	after bone marrow transplantation. Antagonists of the protein may	
CC	CC	be used to suppress the immune system, treat autoimmune diseases,	
CC	CC	including rheumatoid arthritis, multiple sclerosis and diabetes	
CC	CC	melittis. Immune suppression caused by the antagonists can also be	
CC	CC	used to reduce rejection of tissue or organ transplants and grafts,	
CC	CC	and to treat T-cell specific leukaemias and lymphomas.	
XX	SQ	Sequence 623 AA:	
		100.0%: Score 3424; DB 19; Length 623;	
		Best Local Similarity 100.0%; Pred. No. 3,2e-265;	
		Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MNRLVARLTPLLELLSLMSLLIGTRPHGSPGLQCYSGPLGILNCSEPLGDLTPPV 60	
DB	1	mnrLrvarltpllellslmslllgttrphsgpgplqcysvgplgilncswepldgletppv 60	
QY	61	LYHQSKYHNPVRWEVKVSKSWIIPREQFTTMADKLLIWGTQKRPPLWSSVSNLEQT 120	
DB	61	lyhqskqyhnprwvewkvpksqswitpreqfttmadklllwgtdqgrplwssvsnleqt 120	
QY	121	MKPDTPQIFSDQVDSIEATLEAVQWAPPVWPPOKALTQCFYKCEQAAWTRLEPOLKT 180	
DB	121	mkipdtpqifsqvdiseatleavqwapvpwpqokaltcqfrykceqaaawtrlepolkt 180	
QY	181	DGLTPVEMQNLEPGTCYQVSGRCQVNGYPWGESSPLSFQTPFLDPEDVWVSGTYCETS 240	
DB	181	dgltpvemqnlepgtcyqvsgrcqvangypwgewssplsfqtpfldpedvwwsgtycets 240	
QY	241	GKRAALLVWKDPRCPQVQVYTVWFAGDITTTQEEVPCCKSPVPAMWAVVSPGNSTSW 300	
DB	241	gkraallvwkdprcpvqvtytvwfgagdtittqeevpcckspvpamewavvsgpnstsw 300	
QY	301	VPPTNLSLVCLAPESAPCDVGVSADGSPGKVTWKQGRKPLEYVVDNAQDGDSDLKLN 360	
DB	301	vpptnlslvclapesapcdvgvsadgspgikvtwkqgrkpleyvvdwaqgdgdsldkin 360	
QY	361	WTRLPFGNLSTLLPGEFKGQVPIRITVAVYSGGLAAAPSVWGFREELVPLAGPAWRPLP 420	
DB	361	wtrlpfgnlstllpgefkggvpirictvavysgglaaapsvwgfreetvplagpavwrilp 420	
QY	421	DDPPGTPVVAWGEVPRHOLRGQATHYTFCTIOSRGLSTVCERNVSSQFTATLPLNHSSEPK 480	
DB	421	ddppgtpvvaawgevprhqlrgqathytfctiosrglstvcernvssqftatlpnhsgsfk 480	
QY	481	LWTVSTVAGQGGPGLSLHLPDNRIRKALPWFLSLWGLLIMGCLSLASTRCLQARC 540	
DB	481	lwvtvstvagggppgplslhlpdnirwkalpwflslwglimgcslastrclqarc 540	
QY	541	LHWRHKLQWIERVDPDPANSGOPQYIKEVSLPQPKDGPPILEVVEELQPVVESPKA 600	
DB	541	lwhrhklpqwiwervdpdpansugopyikevslpqpkdgpilveeelqpvespka 600	
QY	601	SAPIYSGYEKHFLLPTEELGLLV 623	
DB	601	sapiysgyekhfllptpeeigllv 623	
	RESULT 2		
	AAU01854		
	ID AAU01854 standard; Protein; 623 AA.		
	XX		

AC	AAU01854;		
XX	07-SEP-2001 (first entry)		
DT	Mouse type I cytokine receptor, mTCCR.		
XX	Mouse; type-I cytokine receptor; TCCR; T-cell differentiation;		
KW	Th1; Th2; agonist; antagonist; autoimmune inflammatory disease;		
KW	allergraft rejection; multiple sclerosis; inflammatory bowel disease;		
KW	insulin-dependent diabetes mellitus; infectious disease;		
KW	human immunodeficiency virus; allergic disorder; asthma;		
XX	allergic rhinitis; HIV.		
OS	Mus musculus.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..24	
FT	Modified-site	/label= Signal_peptide	
FT	Region	10..13	
FT	Protein	/note= "Casein kinase II phosphorylation site"	
FT	Region	14..51	
FT	Protein	/note= "Region of homology to human erythropoietin"	
FT	Region	25..623	
FT	Protein	/label= Mature_mTCCR	
FT	Region	36..49	
FT	Modified-site	43..48	
FT	Modified-site	/label= N_myristoylation_site	
FT	Modified-site	46..49	
FT	Modified-site	/note= "Asn is N-glycosylated"	
FT	Modified-site	93..96	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	102..102	
FT	Modified-site	/label= N_myristoylation_site	
FT	Modified-site	130..133	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	172..175	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	184..187	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	202..209	
FT	Region	/note= "Tyrosine kinase phosphorylation site"	
FT	Region	211..219	
FT	Modified-site	/note= "Region of homology with murine interleukin-5 receptor"	
FT	Modified-site	235..238	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	240..245	
FT	Modified-site	/label= Amidation_site	
FT	Modified-site	271..274	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	272..275	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	295..300	
FT	Modified-site	/label= N_myristoylation_site	
FT	Modified-site	296..299	
FT	Modified-site	/note= "Asn is N-glycosylated"	
FT	Modified-site	305..308	
FT	Modified-site	/note= "Asn is N-glycosylated"	
FT	Modified-site	321..326	
FT	Modified-site	/label= N_myristoylation_site	
FT	Modified-site	323..326	
FT	Modified-site	/note= "Casein kinase II phosphorylation site"	
FT	Modified-site	330..335	
FT	Modified-site	/label= N_myristoylation_site	
FT	Modified-site	360..361	
FT	Modified-site	/note= "Asn is N-glycosylated"	
FT	Modified-site	367..372	
FT	Modified-site	/label= N_myristoylation_site	
FT	Modified-site	368..371	
FT	Modified-site	/note= "Asn is N-glycosylated"	
FT	Modified-site	393..398	
FT	Modified-site	/label= N_myristoylation_site	

FT Modified-site 461..464
FT Domain /note= "Asn is N-glycosylated"
FT 514..532
FT /label= Transmembrane_domain
FT Modified-site 516..526
FT /note= "Prokaryotic membrane lipid attachment site"
FT Modified-site 525..530
FT /label= N_myrlistoylation_site
FT Modified-site 527..532
FT /label= N_myrlistoylation_site
FT Modified-site 606..609
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 615..618
FT /note= "Casein kinase II phosphorylation site"
XX
XX WO200129070-A2.
XX
XX 26-APR-2001.
XX
XX 18-OCT-2000; 2000WO-US28827.
XX
XX 20-OCT-1999; 99US-0160542.
XX
XX (GETH) GENENTECH INC.
XX
XX De Sauvage FJ, Grewal I, Gurney AL;
PI WPI; 2001-308474/32.
DR N-PSDB; AAS03263.
XX
XX Modulating T-cell differentiation and cytokine release profiles into
FT Th1 and Th2 subtypes, for treating immune-related diseases in mammals,
FT by administering modulator of type I cytokine receptor (TCR) -
XX
XX Example 1; Fig 4; 126pp; English.
XX
XX The sequence represents mouse type I cytokine receptor, mTCR. The
CC invention relates to methods of modulating the differentiation of
CC T-cells into the Th2 subtype instead of the Th1 subtype, by
CC administering a modulator of TCR (e.g. an antagonist) to enhance,
CC stimulate or potentiate T-cell differentiation, or using TCR
CC polypeptide or its agonists to prevent, inhibit or attenuate T-cell
CC differentiation. Th1 mediated disease in mammal can be treated by
CC administering a TCR antagonist and Th2 diseases by administering a TCR
CC agonist. Th1-mediated diseases include allograft rejection and autoimmune
CC inflammatory diseases, such as allergic encephalomyelitis, multiple
CC sclerosis, insulin-dependent diabetes mellitus, autoimmune uveoretinitis,
CC inflammatory bowel disease or autoimmune thyroid disease. Th2-mediated
CC diseases include infectious diseases, such as Leishmania major,
CC Mycobacterium leprae, Candida albicans, Toxoplasma gondii, respiratory
CC syncytial virus and human immunodeficiency virus (HIV) and allergic
CC disorders, such as asthma, allergic rhinitis, dermatitis and vernal
CC conjunctivitis.
XX
XX Sequence 623 AA;
XX
XX Query Match 100.0%; Score 3424; DB 22; Length 623;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-265;
XX Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 MNRRLVRLTLELLLSLMSLLGTRPHGSPGLQCYSGVPLGLNCSWEPLGDLTEPPV 60
XX
XX 1 mnrilvrltplelllsllmslllgrphgspgplqcyvgplglncswepglgdlteppv 60
XX
XX 61 LYHQSQKYPNRRVWEKVPKQSWWTIPREQFTMDKLLIWTQKGRPLWSVSVNLETQ 120
XX
XX 61 lyhgsqkyhpnrrvwekvpskswwtipreqftmdklllwtqkgrplwssvsnletq 120
XX
XX 121 MKPDTPTQIFSQVDISEEATLEATVQWAPPVPPQKALTCQRYKCEQAEATRLPEQLKT 180
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XX 121 mkpdtptqifsqvdiseeatleatvqwapppvppqkaltcqrykceqaeatrlpeqlkt 180

Qy 181 DGLTPVEMQNLEPGTCYQVSGRCQVENGYPMGEMSSPLSFQTPFLDPEDVWVSGTVCETS 240
Db 181 dgltpvemqnlpgtscyqvgvgrcqvengypmgewssplsfqtpfldpedvwwsgtvcets 240
Qy 241 GKRAALLVWKDPRPCVQVYTYVWFCAGDITTTQBEVPCKCKSPVPAWMEHAWVSPGNSISW 300
Db 241 gkraallvwkdprpcvqvtytwfagaditttqbevpckckspvpawmewavvsgnsw 300
Qy 301 VPPTNLSLVCLAPESAPCDVGVSSADGSPGKIVTKQGTGRKPLEYVVDMAQDGLSLDKLN 360
Db 301 vpptnlsivclapesapcdvgvssadgspgkivtkqgtrkpleyvvvdaqdgldkl 360
Qy 361 WTRLPPGNLSTLLPGEFKGGVPYRITVAVYSGGLAAAPSVWGFREELVPLAGPAVWRUP 420
Db 361 wtrlppgnlstllpgfefkggvpyritvavysgglaaapsvwgfreelvplagpavwrup 420
Qy 421 DDPGTTPVWANGVEPRHOLRGOATHYTCIQSRGLSTVCRNVSSQTATLNLHSGSFK 480
Db 421 ddpghtpvwangevprholrgoathyticqsrglstvcrnvssqtatlnlhsgsfk 480
Qy 481 LWVTYSTVAGOGPPGDLSLHLPDNRIRWKPFLSLWGLLMLGGLSLASTRCLQARC 540
Db 481 lwtvtystvagogppgdlslhlpdnrirkwkalpwlslwglmlgglslastrclqarc 540
Qy 541 LHWHRKLLPQMIWIRVDPDANSNSGQPYIKEYSLPQPKDGPILVEVEYELQPVVESPKA 600
Db 541 lwhrhkllpqmiwirvdpdansnsgpyikevslppqkdgpilveeveelqpvvespka 600
Qy 601 SAPIYSGYEKHFLLPTPEELGLLV 623
Db 601 sapiysgyekhfllptpeelgilv 623
RESULT 3
AAW33399
ID AAW33399 standard; Protein; 636 AA.
AC AAW33399;
XX
XX 22-MAY-1998 (first entry)
XX
XX Alternatively spliced zcytor1.
XX
XX Human; haematopoietic cytokine receptor; zcytor1; ligand detection;
XX cancer diagnosis; agonist; antagonist; alternatively spliced.
XX Homo sapiens.
XX
XX WO9744455-A1.
XX
XX 27-NOV-1997.
XX
XX 19-MAY-1997; 97WO-US08502.
XX
XX 23-MAY-1996; 96US-0653740.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;
XX
XX WPI; 1998-018509/02.
XX
XX N-PSDB; AAT94120.
XX
XX Haematopoietic cytokine receptor - useful for ligand detection, and
XX pathological condition diagnosis
XX
XX Claim 7; Pages 46-51; 86pp; English.
XX
XX The present sequence is an alternatively spliced human
XX haematopoietic cytokine receptor zcytor1, useful for ligand
XX detection, and pathological condition diagnosis, including cancer.
XX Receptor agonists of the protein can be used to stimulate the
XX proliferation and development of target cells in vitro and in vivo.

CC The agonists can stimulate cell mediated immunity and lymphocyte
CC proliferation, to treat infection involving immunosuppression, e.g.
CC viral infections. They may also be used to suppress tumours, induce
CC cytotoxicity, treat leukopenias and enhance the regeneration of
CC the T-cell repertoire after bone marrow transplantation.
CC Antagonists of the protein may be used to suppress the immune
CC system, treat autoimmune diseases, including rheumatoid arthritis,
CC multiple sclerosis and diabetes mellitus. Immune suppression caused
CC by the antagonists can also be used to reduce rejection of tissue
CC or organ transplants and grafts, and to treat r-cell specific
CC leukaemias and lymphomas.

xx
SQ Sequence 636 AA;

Query Match 59.7%; Score 2044; DB 19; Length 636;
Best Local Similarity 62.8%; Pred. No. 6.7e-155;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

QY 9 LTPLELLSLMSLLGTRPHGSPGLQCYSGPLGLINGSWEPGLDTPPPVLYHQSQRY 68
Db 14 lpklallpllwlfqtrpgsgugplqcygvpplgdlncswepplgdlgapsehlqsgky 73
QY 69 HPNRWVEVYKQSQWYTPREQFTWADKLLINGTQKGRPLWSSVSNLETKMKPTPOI 128
Db 74 rsnktqtvaagrswwaipreqltmsdkllwgtkagqplwppvfnletgmknapz1 133
QY 129 FSOVDISEATLEATVQWAPVPPVPPKATCFPRYKCCQAEATWLPOLKTDGLTPVEM 188
Db 134 gpdvdfseddpaleatwhaprtwpskhvlicqfhyrcqeaawlllepelktpiltpvel 193
QY 189 QNLEPTCYQVSGRCOVENGYP-WGSWSSPLSQTPFLDPEDVWVSCTVCTSGKRAALL 247
Db 194 qdilelatgkyvgrcmekedlwgespllsftqpsapkdvwsngnlicgtgpggepll 253
QY 248 VKMDPRPCQVYTVWFGAGDITTTQEEVPCCKSPVPAWENAVSPGNSTSWPPTNLS 307
Db 254 lwkapgpcvqsykvfwggralspegitcccllpsgaewarvsavnatwspeptnls 313
QY 308 LVCLAPESAPCDVGSASDGSPIKVTWKGTRKPLEYVVDNAQDGLDKLWTRLPFG 367
Db 314 lvcldasaprsvavasagstetllvtwqpgpgeplehvvdwardgplekinwvrlppg 373
QY 368 NLSTLLPFGFKGVPYRIYTVAVISGLAAPSVMGFRLEELVPLAGPVMVRLPDDPPGTP 427
Db 374 nlsallpgnftvgpyrlctvavsaaglasasswvfreelaplvgtplwrlqadpgtp 433
QY 428 VWANGVPRHQLRGQATHYTFQTSRGLSTVCRNVSSQTATLPNLHSGSKLWTVTST 487
Db 434 alawgevprhqlrghlthylclsqsgtspscmvnvgntqsvtlpdlwpgpcelwvtast 493
QY 488 VAGQGPFGPDLSLHLPDNRIRKALPWFSLMGLLLMGGLSLASTPCLQARCLHWRHL 547
Db 494 iagggppgplrlhupdntrkwpilgllfwgflilgclslats---grcyhlrhkv 549
QY 548 LPQWIERVDPDANSNGOPYIKEVSLPPKDPKDPILVEVEVELOQPVVES---PKASAPI 604
Db 550 lprwvkwkvpdpansngpshmeqveacplgdlplveemepppvmesspaqatapl 609
QY 605 YSGYKHFLPTPEELGLL 622
Db 610 dsgyekhflptpeelgll 627

RESULT 4
AAU01853
ID AAU01853 standard; Protein; 636 AA.
XX
AC AAU01853;
XX
DT C7-SEP-2001 (first entry)
XX Human type I cytokine receptor, hTCCR.

xx
KW Human; type-I cytokine receptor; TCCR; T-cell differentiation;
KW Th1; Th2; agonist; antagonist; autoimmune inflammatory disease;
KW allograft rejection; multiple sclerosis; inflammatory bowel disease;
KW insulin-dependent diabetes mellitus; infectious disease;
KW human immunodeficiency virus; allergic disorder; asthma;
KW allergic rhinitis; HIV.
OS Homo sapiens.

xx
FH Key Location/Qualifiers
FT Peptide 1..32
FT Protein 33..636
FT /label= Signal_peptide
FT /label= Mature_hTCCR
FT Region 41..54
FT /note= "Cytokine receptor family signature 1"
FT Modified-site 51..54
FT /note= "Asn is N-glycosylated"
FT Modified-site 76..79
FT /note= "Asn is N-glycosylated"
FT Modified-site 107..112
FT /label= N-myristoylation_site
FT Region 183..191
FT /note= "Region of homology with the second subunit
FT of human granulocyte-macrophage colony-stimulating
FT factor"
FT Modified-site 240..245
FT /label= N-myristoylation_site
FT Modified-site 244..249
FT /label= N-myristoylation_site
FT Modified-site 281..286
FT /label= N-myristoylation_site
FT Modified-site 292..297
FT /label= N-myristoylation_site
FT Modified-site 302..305
FT /note= "Asn is N-glycosylated"
FT Modified-site 311..314
FT /note= "Asn is N-glycosylated"
FT Modified-site 373..378
FT /label= N-myristoylation_site
FT Modified-site 374..377
FT /note= "Asn is N-glycosylated"
FT Modified-site 382..385
FT /note= "Asn is N-glycosylated"
FT Modified-site 400..405
FT /label= N-myristoylation_site
FT Modified-site 439..464
FT /label= N-myristoylation_site
FT Modified-site 467..470
FT /note= "Asn is N-glycosylated"
FT Modified-site 470..475
FT /label= N-myristoylation_site
FT Domain 517..538
FT /label= Transmembrane_domain
FT Modified-site 522..532
FT /note= "Prokaryotic membrane lipid attachment site"
FT Modified-site 531..536
FT /label= N-myristoylation_site
FT Modified-site 533..538
FT /label= N-myristoylation_site
FT Modified-site 563..566
FT /note= "Asn is N-glycosylated"
xx
PN WO200129070-A2.
xx
PD 26-APR-2001.
xx
PF 18-OCT-2000; 2000WO-US28827.
xx
PR 20-OCT-1999; 99US-0160542.
xx
PA (GETH) GENENTECH INC.

XX De Sauvage FJ, Grewal I, Gurney AL;
XX WPI; 2001-308474/32.
XX N-PSDB; AAS03262.
XX
XX Modulating T-cell differentiation and cytokine release profiles into
XX Th1 and Th2 subtypes, for treating immune-related diseases in mammals,
XX by administering modulator of type I cytokine receptor (TCR) -
XX
XX Example 1; Fig 3; 126pp; English.
XX
XX The sequence represents human type I cytokine receptor, hTCR. The
XX invention relates to methods of modulating the differentiation of
XX T-cells into the Th2 subtype instead of the Th1 subtype, by
XX administering a modulator of TCR (e.g. an antagonist) to enhance,
XX stimulate or potentiate T-cell differentiation, or using TCR
XX polypeptide or its agonists to prevent, inhibit or attenuate T-cell
XX differentiation. Th1 mediated disease in mammal can be treated by
XX administering a TCR antagonist and Th2 diseases by administering a TCR
XX agonist. Th1-mediated diseases include allograft rejection and autoimmune
XX inflammatory diseases, such as allergic encephalomyelitis, multiple
XX sclerosis, insulin-dependent diabetes mellitus, autoimmune uveoretinitis,
XX inflammatory bowel disease or autoimmune thyroid disease. Th2-mediated
XX diseases include infectious diseases, such as Leishmania major,
XX Mycobacterium leprae, Candida albicans, Toxoplasma gondii, respiratory
XX syncytial virus and human immunodeficiency virus (HIV) and allergic
XX disorders, such as asthma, allergic rhinitis, dermatitis and vernal
XX conjunctivitis.
XX
XX Sequence 636 AA;
SQ

Query Match 59.7%; Score 2044; DB 22; Length 636;
Best Local Similarity 62.8%; Pred. No. 6.7e-155;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

QY 9 LTPLELLLSMLLGLTRPHSGPLQCYSVGLGILNCSEWPLGLDLETPPVLYHQSKY 68
DB 14 lpkalllpilwlfqtrtrpgsagplqcygvgplgdlncswepldgldgapselhlqskq 73
QY 69 HPNRVWEVKVPSKOSWTIPREQTMDKLLIWTQGRPLWSSVNLFTQMPTDPOI 128
DB 74 rsnktqtvaagrsvaipreqtlmsdkllvgtkagqplwppfvnletqmkpnael 133
QY 129 FSOVDISEATLEATVQWAPPVPPQKALTCOPRYKCOAEATWRLPQLKTDGLTPVEM 188
DB 134 gpdvdfsedpleatvhwaptwshkvilcqhfyrrcqeaawtllepelktipltpvei 193
QY 189 QNLEPGTCYQVSGRCQVNGYP-WGEWSSPLSFQTPFLDPEDVWVSGTVCETSGKRAALL 247
DB 194 qdlelatgkyvycrmekeedlgewspilsfqtpspakdvwvsgnlcgtpggeep 253
QY 248 WKDPRCVQYTVWFGAGDITTTQEVPCCKSPVPAWMEAVVSPGNSTSWPTNLS 307
DB 254 lkwagpgcvqsvykwvwtvggrelspesgitccclipsagaewarvsavnatsepltnls 313
QY 308 LVCLAPESAPCDVGSADSPGKIVTWKQGRKPLEVVDWADGDSLDKLNWRLPPG 367
DB 314 lvcldasasprsvasslagsteltvtpgpgpleinvdwardgdpleklnwrlppg 373
QY 368 NLSTLLPFEKGGVPIRYTAVYSGGLAAPSVMGFREELVPLAGPAWRLPDDPGTP 427
DB 374 nlsallpncfvcyprytvavsglasassvvgfreelaplvgptlwrldappetp 433
QY 428 VVANGEPVRLQQAHTYFCISGRGLSTVCRNVSSQTATPLNLHSGSEKLVWTVST 487
DB 434 aiagvevprhlqrlhlytlcadsgtspscmvnsgntqsvtlpdlpwgpcelwvtast 493
QY 488 VAGOGPPGDLSLHLPDNRTRWKLWFLSLWGLLLMGCGLSLASTCLQARCLHWRHKL 547
DB 494 iagggpppilirhlpdntlrwklwpgllfwlglgclslats-----grcyhlrhkv 549

QY 548 LPQWTWVRPDPANSSGOPYIKESVLPQPPKDGPILEVVEVLEQPVVES---PKASAPI 604
DB 550 lprwwwkvdpdpanssgphmeqveapldglpilleveempppvmesspaqatapl 609
QY 605 YSGYEKHEFLPTPEELGLL 622
DB 610 dsgyekhflptpeeigl 627
RESULT 5
RAY29781
ID AAY29781 standard; Protein; 636 AA.
XX
XX AAY29781;
XX
XX 04-NOV-1999 (first entry)
XX Human DNAX cytokine receptor subunit 1.
XX DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
XX interleukin B30; DSRs1; DCRs1; IL-B30; cytokine receptor; diagnosis;
XX inflammatory disorder; inflammatory response; innate immunity;
XX morphogenic development; immunological disorder.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 108 /label= unknown
XX /note= "encoded by AYT"
XX
XX WO9940195-A1.
XX
XX 12-AUG-1999.
XX
XX 05-FEB-1999; 99WO-US02600.
XX
XX 13-MAY-1998; 98US-0078194.
XX 06-FEB-1998; 98US-0073941.
XX (SCHE) SCHERING CORP.
XX Kastelein RA, Mattson JD, McClanahan TK;
XX WPI; 1999-527306/44.
XX N-PSDB; AAZ08863.
XX
XX New receptor subunits useful in the treatment inflammatory disorders
XX
XX Claim 2; Page 14-17; 133pp; English.
XX
XX The present invention describes a composition (I) comprising DNAX
XX cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
XX subunit I (DSRS1) protein, which together encode a new mammalian
XX cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)
XX proteins, or DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRS1
XX is useful for screening for ligands (i.e. agonists/antagonists) from
XX a library of compounds, which are useful for modulating the physiology
XX or development of a cell or tissue culture e.g. inflammatory responses,
XX innate immunity and/or morphogenic development. (R), antibodies and
XX ligands are useful for treatment of conditions, especially immunological
XX disorders, associated with conditions exhibiting abnormal expression of
XX (R). (R) is useful as a phosphate labeling enzyme to label substrates,
XX and the subunits DSRs1 and DCRS1 are useful as immunogens for generating
XX antibodies, or as antigens for binding antibodies. Nucleic acids
XX encoding (R) are useful for identifying related DNAs and mRNAs, and
XX variants from other individuals or species. The present sequence
XX represents the specifically claimed human DCRS1, for use in the
XX composition of the present invention.
XX
XX Sequence 636 AA;
SQ

Query Match	59.5%;	Score	2036;	DB	20;	Length	636;
Best Local Similarity	62.5%;	Pred.	No. 2.9e-154;				
Matches	386;	Conservative	62;	Mismatches	162;	Indels	8;
Gaps	3;						
Qy	9	LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGLNCSWEPLGDLETPPVLYHQSQKY	68				
Db	14	lpklallpllwlfgrtrpqgsagplqcyvgplgdlncswepldgapselhlqsky	73				
Qy	69	HPNRVWEVKVPKSWITIPRQFTMADKLLIWGTQKGRPLWSSVSNLETKMPTPOI	128				
Db	74	rsnktqtvaagrsawalpreqltmsdkllwvgkagqplwppvfnletgmknapi	133				
Qy	129	FSQVDISEATLEATVQWAPPVPPQKALTCQFRYKECAEAWTRLEPOLKTDGTPVEM	188				
Db	134	gpdvfdsedpleatvhwappwshkvlicqfhyrrcqeaawtllpeelktiptvei	193				
Qy	189	QNLEPGTCYQVSGRCQVGENYP-WGEWSSPLSFQTFPLDPEDVWVSGTVCETSGKRAALL	247				
Db	194	qdeleatgykyvgrcmekeedlwgeaspilfsqtpspakdvwvsgnlcgtpggeep	253				
Qy	248	VNKDPRPCVQVITYWFGAGDITTTQEEVPCCSPVPAMWNAVSPGNSTSWVPPTNLS	307				
Db	254	lwkagpcqvskykfwvvggrelspegitcccsilpsgaeavrsavnatsewptnls	313				
Qy	308	LVCLAPESAPCDVGVSSADGSPGIKVTWKQTRKPLEYVVDWAQDGLDKLNWTRLPPG	367				
Db	314	lvcldsasaprsvavssilagsteillvtwpgpgpelehmvdwardgdpleklnwrlppg	373				
Qy	368	NLSTLLPGFEKGVPRITVTAVYSGGLAAAPSVWGFREELVPLAGPAVMRLPDDPPGTP	427				
Db	374	nlsallpgnftvgvpyrlvtavssaglasassvvgffeelaplvgptlwrldqappgcp	433				
Qy	428	VYAWGEVPRHQURGOATHYTFCIQSRGLSTVCRNVSSQTQTATLPNLHSGSFKLWTVST	487				
Db	434	alawgevrhqlrghlthyltcaqgstpsvcmvsgntqstvtlplwpgpcelwvtast	493				
Qy	488	VAGQPGPDLSLHLPDNRIRWKALPWFLSLWGLLLMGCGLSLASTRCLQARCLHWRHKL	547				
Db	494	iagggppgilrlhlpdntlrwkvlpglflwglfllgcglalats---grcyhlrhkv	549				
Qy	548	LPQWIERVPDPANSSGOPYIKVSLPQPPKDGPILEVEEVELOPVVES---PKASAPI	604				
Db	550	lprwwekvpdpansssgqphmeqvpeaqplgdplileveempppvnmessqagatapi	609				
Qy	605	YSGYEKHFLLPTPEELGLL	622				
Db	610	dsgyekhfllptpeelgl	627				
RE	6						
AAW33398							
ID	AAW33398	standard; Protein; 578 AA.					
XX							
AC	AAW33398;						
XX							
DT	22-MAY-1998	(first entry)					
DE		Human haematopoietic cytokine receptor zcytor1.					
XX							
KW		Human; haematopoietic cytokine receptor; zcytor1; ligand detection;					
KW		cancer diagnosis; agonist; antagonist.					
OS		Homo sapiens.					
XX							
PN	WO9744455-A1.						
XX							
PD	27-NOV-1997.						
XX							
PF	19-MAY-1997;	97MO-US08502.					
XX							
PR	23-MAY-1996;	96US-0653740.					
XX							
PA	{ZIMO } ZYMOGENETICS INC.						

XX			
PI	Baumgartner JW,	Foster DC,	Grant FJ, Sprecher CA;
XX			
DR	WPI: 1998-018509/02.		
DR	N-PSDB; AAT94119.		
XX			
PT	Haematopoietic cytokine receptor - useful for ligand detection, and		
PT	pathological condition diagnosis		
XX			
PS	Claim 1; Pages 39-43; 86pp; English.		
XX			
CC	The present sequence is the human haematopoietic cytokine		
CC	receptor zcytor1, useful for ligand detection, and pathological		
CC	condition diagnosis, including cancer. Receptor agonists of the		
CC	protein can be used to stimulate the proliferation and development		
CC	of target cells in vitro and in vivo. The agonists can stimulate		
CC	cell mediated immunity and lymphocyte proliferation, to treat		
CC	infection involving immunosuppression, e.g. viral infections. They		
CC	may also be used to suppress tumours, induce cytotoxicity, treat		
CC	leukopaenias and enhance the regeneration of the T-cell repertoire		
CC	after bone marrow transplantation. Antagonists of the protein may		
CC	be used to suppress the immune system, treat autoimmune diseases,		
CC	including rheumatoid arthritis, multiple sclerosis and diabetes.		
CC	melittis. Immune suppression caused by the antagonists can also be		
CC	used to reduce rejection of tissue or organ transplants and grafts,		
CC	and to treat T-cell specific leukaemias and lymphomas.		
XX			
SQ	Sequence	578 AA;	
	Query Match	54.5%;	Score 1866.5; DB 19; Length 578;
	Best Local Similarity	61.7%;	Pred.No. 9e-141;
	Matches	353;	Conservative 53; Mismatches 153; Indels 13; Gaps 3;
Qy	9	LTPLELLLSMLLLGTRPHGSPGLQCYSGVPLGLNCSWEPLGDLETPPVLYHQSQKY	68
Db	14	lpklallpllwlfgrtrpqgsagplqcyvgplgdlncswepldgapselhlqsky	73
Qy	69	HPNRVWEVKVPKSWITIPRQFTMADKLLIWGTQKGRPLWSSVSNLETKMPTPOI	128
Db	74	rsnktqtvaagrsawalpreqlmsdkllwgtkagqplwppvfnletgmknapi	133
Qy	129	FSQVDISEATLEATVQWAPPVPPQKALTCQFRYKECAEAWTRLEPOLKTDGTPVEM	188
Db	134	gpdvfdsedpleatvhwappwshkvlicqfhyrrcqeaawtllpeelktiptvei	193
Qy	189	QNLEPGTCYQVSGRCQVGENYP-WGEWSSPLSFQTFPLDPEDVWVSGTVCETSGKRAALL	247
Db	194	qdeleatgykyvgrcmekeedlwgeaspilfsqtpspakdvwvsgnlcgtpggeep	253
Qy	248	VNKDPRPCVQVITYWFGAGDITTTQEEVPCCSPVPAMWNAVSPGNSTSWVPPTNLS	307
Db	254	lwkagpcqvskykfwvvggrelspegitcccsilpsgaeavrsavnatsewptnls	313
Qy	308	LVCLAPESAPCDVGVSSADGSPGIKVTWKQTRKPLEYVVDWAQDGLDKLNWTRLPPG	367
Db	314	lvcldsasaprsvavssilagsteillvtwpgpgpelehmvdwardgdpleklnwrlppg	373
Qy	368	NLSTLLPGFEKGVPRITVTAVYSGGLAAAPSVWGFREELVPLAGPAVMRLPDDPPGTP	427
Db	374	nlsallpgnftvgvpyrlvtavssaglasassvvgffeelaplvgptlwrldqappgcp	433
Qy	428	VYAWGEVPRHQURGOATHYTFCIQSRGLSTVCRNVSSQTQTATLPNLHSGSFKLWTVST	487
Db	434	alawgevrhqlrghlthyltcaqgstpsvcmvsgntqstvtlplwpgpcelwvtast	493
Qy	488	VAGQPGPGLSLHLPDNRIRKALPWFLSLWGLLMGGLSLASTRCLQARCLHWRHKL	547
Db	494	iagggppgilrlhipdntlrwkvlpglflwglfllgcglalats---grcyhlrhkv	549
Qy	548	LPQWIERVPDPANSSGOPYIKVSLPQPPKDGPILEVEEVELOPVVES---PKASAPI	604
Db	550	lprwwekvpdpansssgqphmeqvpeaqplgdplileveempppvnmessqagatapi	609


```
CC innate immunity and/or morphogenic development. (R), antibodies and
CC ligands are useful for treatment of conditions, especially immunological
CC disorders, associated with conditions exhibiting abnormal expression of
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,
CC and the subunits DSRs1 and DCRs1 are useful as immunogens for generating
CC antibodies, or as antigens for binding antibodies. Nucleic acids
CC encoding (R) are useful for identifying related DNAs and mRNAs, and
CC variants from other individuals or species. The present sequence
CC represents the partial mouse DCRs1, given in the present invention.
XX
SQ Sequence 246 AA;

Query Match 39.2%; Score 1342; DB 20; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.3e-99;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 378 KGVPRYITVTAVYSGGLAARSVGFRRELYPLAGPAWRPLDDPGTPVVAWGEVPRH 437
DQ 1 KGGVPYRITVTAVYSGGLAARSVGFRRELYPLAGPAWRPLDDPGTPVVAWGEVPRH 60
QY 438 QLRGQATHYFCIQRGLSTVCVRNYSSTQTATPLNLHSGSKLWTVSTVAGQGGPPGD 497
DB 61 qlrgqathyfcicqrglstvcvrnysvsgqqtatplnlhsgsklwtvstvcvggppgd 120
QY 498 LSLHLPDNRIRKALPWFUSLWGLLMLGCLSLASTRCLOARCLHWRHKLPLQWIWERYP 557
DB 121 lslhlpdnrirkalpwwfslwglmlgclslastrclqarclhwrhklplqwiewerp 180
QY 558 DPANNSGGPYLKEVSLPPDKCPLEVEVEVELQPVVSPKASAPIYSGYKHFLPTPE 617
DB 181 dpannsqgpylkevsllppdkdgpillevevelqpvvespkasapiysgyekhflptpe 240

QY 618 ELGLLV 623
DB 241 elgllv 246

RESULT 9
ID AAY29782
XX
AC AAY29782;
XX
DT 04-NOV-1999 (first entry)
XX
DE Mouse DNAX cytokine receptor subunit 1.
XX
KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
KW Interleukin B30; DSRs1; DCRs1; IL-B30; cytokine receptor; diagnosis;
KW inflammatory disorder; inflammatory response; innate immunity;
KW morphogenic development; immunological disorder.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 150
FT /label= unknown
FT /note= "encoded by GAN"
XX
PN WO9940195-A1.
XX
PD 12-AUG-1999.
XX
PF 05-FEB-1999; 99WO-US02600.
XX
PR 13-MAY-1998; 98US-0078194.
XX
PR 06-FEB-1998; 98US-0073941.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Kastelein RA, Mattson JD, McManahan TK;
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DR WPI; 1999-527306/44.
DR N-PSDB; AA208864.
XX
PT New receptor subunits useful in the treatment inflammatory disorders
XX
PS Claim 2; Page 17-18; 133pp; English.
XX
CC The present invention describes a composition (I) comprising DNAX
CC cytokine receptor subunit I (DCRs1) protein and DNAX soluble receptor
CC subunit I (DSRs1) protein, which together encode a new mammalian
CC cytokine-related receptor (R), or DCRs1 and interleukin B30 (IL-B30)
CC proteins, or DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRs1
CC is useful for screening for ligands (i.e. agonists/antagonists) from
CC a library of compounds, which are useful for modulating the physiology
CC or development of a cell or tissue culture e.g. inflammatory responses,
CC innate immunity and/or morphogenic development. (R), antibodies and
CC ligands are useful for treatment of conditions, especially immunological
CC disorders, associated with conditions exhibiting abnormal expression of
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,
CC and the subunits DSRs1 and DCRs1 are useful as immunogens for generating
CC antibodies, or as antigens for binding antibodies. Nucleic acids
CC encoding (R) are useful for identifying related DNAs and mRNAs, and
CC variants from other individuals or species. The present sequence
CC represents the specifically claimed mouse DCRs1, for use in the
CC composition of the present invention.
XX
SQ Sequence 150 AA;

Query Match 20.8%; Score 712; DB 20; Length 150;
Best Local Similarity 98.5%; Pred. No. 2.7e-49;
Matches 133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNRLRVARLTPLLELLSLMSLLGLTRPHGSPGLQCYSGPLGILMCSWEPLDLETPPV 60
DB 15 mnrlrgarltpllellslmslllgltrphgspgplqcyvgplilncswepldletppv 74
QY 61 LYHQSKYHPNRVWEVKVPSKOSWVTIPREQFTMAKLLIWTQKGRPLMSSVSVNLETQ 120
DB 75 lyhqskqyhpnrwvevkvpksgwvtipreqftmadklllwtgkgrplwssvsvnletq 134
QY 121 MKPDTPOIFSOVDIS 135
DB 135 mkpdtppqifsqvdis 149

RESULT 10
AAW12771
ID AAW12771 standard; Protein; 862 AA.
XX
AC AAW12771;
XX
DT 12-MAY-1997 (first entry)
XX
DE Human interleukin-12 beta-2 receptor.
XX
KW Interleukin-12 beta-2 receptor; IL-12; autoimmune disease;
KW rheumatoid arthritis; inflammatory bowel disease;
KW multiple sclerosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide
FT Domain 24..622
FT /label= Extracellular_domain
FT Domain 623..646
FT /label= Transmembrane_domain
FT Domain 647..862
FT /label= Cytoplasmic_tail
FT Region 132..145
FT /label= Cytokine_receptor_motif
```


FT Protein 45..1001 /label Mature_peptide

XX WO9210570-A.

XX 25-JUN-1992.

XX 05-DEC-1991; 91WO-US09112.

XX 13-DEC-1990; 90US-0626725.

XX 13-MAR-1991; 91US-0670608.

XX (IMMV) IMMUNEX CORP.

XX Beckmann MP, Gearing DP;

XX WPI: 1992-234626/28.

XX N-PSDB; AAQ25799.

XX New leukaemia inhibitory factor receptor proteins - for treating

XX LIF-dependent leukaemia, lipoprotein, bone and calcium metabolism

XX defects e.g. atherosclerosis, obesity etc.

XX Disclosure: Page 28-32; 49pp; English.

XX The sequence given is a leukemia inhibitory factor (LIF)-receptor

XX (LIF-R). LIF-R proteins are present on the surface of various

XX hematopoietic and non-hematopoietic cells. They are capable of

XX binding LIF molecules. They are mammalian plasma membrane proteins

XX and play an important role in transducing the signal provided by LIF

XX to a cell. This protein has a molecular weight of approx. 190,000 kD.

XX LIF-R proteins can be used to competitively bind LIF and thereby

XX inhibit its binding to cell surface receptors. Soluble LIF-R may be

XX used in therapy to inhibit the effects of LIF-induced cachexia in

XX cancer patients to treat lipoprotein metabolism defects such as

XX atherosclerosis and obesity. It may also be useful in the treatment

XX of disorders of bone and calcium metabolism or disorders associated

XX with LIF overproduction associated with hepatocytes, neurons and

XX leukocytes.

XX Sequence 1001 AA;

Query Match 8.2%; Score 280; DB 13; Length 1001;

Best Local Similarity 21.5%; Pred. No. 1.2e-13;

Matches 142; Conservative 110; Mismatches 264; Indels 144; Gaps 35;

QY 27 PHGSPGLOQYSGVPLGILNCSWEP-----LGDLETPPVLYHQ-SQKYHPRVWEVKVP 79

DB 332 pPdtPqqlnc-ethdlikeicawmrvrtalvgpratsytlvestsgky--vrlkraeap 388

QY 80 SKQSW---VTIPREQ---FTWADKLLIWGTQGRPL---WSSVSVNLETQMKPDPQPQIF 129

DB 389 tnesyqlfqlmpnqenynftl-----nahmplgrsqstlilvnteikvyphtptsf 439

QY 130 SQVDISEATLEATVQMAPVPVMPKQALTCQFRYKQCAEAMTRLEPQLKTDGLTP---- 185

DB 440 kvkdlnsta---vklswhlpgnfakinficeikksns---vqeqrntikgvessyl 493

QY 186 VEMQNLEPCTCQVSGRCQVENCYPKGENSSPLSFOTPLDPE---DVWVSGTVGCTSGK 242

DB 494 valdklnpytlyfrircstetfvrkswksnkkhlitteespskgpdtw-----rewsdd 548

QY 243 RAALLWKDPRPCVQ-----VVTYVWFAGDITTTQEEVPCCKSPVPANWE-----WAVV 292

DB 549 gknliyskplpneangkilsvnscsdeetqslseipdpqhkaqrlidkndyisvv 608

QY 293 SPGNSTSWVPNTLSLVCLAPESAPCDVGVSSADG-SPGIKVTWKQGRKRPLEYVVDNAQ 351

DB 609 ak-nsvgssppskia-----smeipnddlkieqvvgmgkgilltnhydpmtcdyvikwn 663

QY 352 DGDSDLKL-NWTRLPCNLSTLLPG-EFKGGVPYRTVTAVYSGGLAAPSVWGFREELY 409

Db 664 ssrsepclmdwtkvpsnstetviesdefprgiryfnflygrnqgyqlrlrmigyleela 723

QY 410 PLAGPAVWRLPDDPGTPTVVAMGEVPRHQLRGQATHVTF-----CQSRGLS 456

Db 724 pivapn-ftvedtsadslvkwedipveelrgflrlyfyfkgkgrdtksmrviesgrsd 782

QY 457 TVCRNVSSQTQ-TATLNLH-SGSFKLWTVTVAGQPPGDLSLHL--PDNRIRWKAL 512

Db 783 ikvknitdisqktlriadiqgktsyhlvrayt---dggvgpeksmvvyvckensv----- 834

QY 513 PWFSLWGLL-----LMCGGLSLASTRCQARCLHWRHKLPLPQWIWER----VP 557

Db 835 -----glliaillpavavivgv---vtsilicyrkr-----ewiketfypdip 874

QY 558 DPANSNS-----GQPVKEVSL-PQPPKDGPILE-----VVEVE-LQPVVESPK 599

Db 875 npenckalqfksvcegsaalkleinpctpnnevletrsafpkiedtelispaerpe 934

RESULT 12

AAAR49508

ID AAR49508 standard; Protein; 1097 AA.

XX AC AAR49508;

XX DT 07-JUL-1994 (first entry)

XX DE Human LIF-R.

XX KW LIF-R; leukemia inhibitory factor receptor.

XX OS Homo sapiens.

XX FH Key

XX FT Peptide

XX FT Domain

XX FT Region

XX FT Domain

XX FT Domain

XX US5284755-A.

XX PD 08-FEB-1994.

XX PF 13-DEC-1990; 90US-0626725.

XX PR 13-DEC-1990; 90US-0626725.

XX PR 13-MAR-1991; 91US-0670608.

XX PR 11-SEP-1992; 92US-0943843.

XX PA (IMMV) IMMUNEX CORP.

XX PI Beckmann MP, Gearing DP;

XX DR WPI: 1994-056341/07.

XX DR N-PSDB; AAQ58427.

XX DNA encoding leukaemia inhibitory factor receptor - esp. soluble

XX receptor, used as competitive inhibitor of LIF binding to cell

XX surface, in therapy, diagnosis and assays

XX Disclosure: Column 63-64 to 69-70; 44pp; English.

XX Plasmid pHLIFR-65 (ATCC 68491) includes human placental LIF-R cDNA

XX (given in AAQ58425) encoding a C-terminal truncated LIF-R protein

XX (AAR49506). Screening of human cDNA and genomic libraries using this

XX cDNA yielded composite sequence AAQ58427 encoding full-length human

XX LIF-R (AAR49508). cDNA of sequence AAQ58426, encoding mouse LIF-R

XX (AAR49507), was obtained by screening a liver cDNA library with a human

XX LIF-R probe. A soluble human LIF-R/Fc homodimer can be prepared

FT XX /note= "Potential N-linked glycosylation site."
XX PN US284755-A.
XX PD 08-FEB-1994.
XX XX 13-DEC-1990; 90US-0626725.
XX PF 13-DEC-1990; 90US-0626725.
XX PR 13-MAR-1991; 91US-0670608.
XX PR 11-SEP-1992; 92US-0943843.
XX XX (IMV) IMMUNEX CORP.
XX PA Beckmann MP, Gearing DP;
XX PI WPI: 1994-056341/07.
XX DR N-PSDB; AAQ55942.
XX DR N-PSDB; AAQ55942.
XX PR DNA encoding leukaemia inhibitory factor receptor - esp. soluble
XX PT receptor, used as competitive inhibitor of LIF binding to cell
XX PS surface, in therapy, diagnosis and assays
XX PS Claim 1; Figure 2; 44pp; English.
XX CC Soluble forms of the leukaemia inhibitory factor receptor (LIFR)
CC having the transmembrane domain deleted can be used in therapy,
CC diagnosis, in assays for LIF or LIFR, or for raising antibodies to
CC LIFR. Soluble LIFR proteins can be used for competitive inhibition
CC of binding of LIF to cell surface receptors. Conditions which could
CC benefit from such inhibition include LIF-induced cachexia in cancer
CC patients and lipoprotein metabolism disorders such as
CC atherosclerosis and obesity. Soluble LIFR is also useful in the
CC treatment of disorders of bone and calcium metabolism as well as
CC those associated with the over production of LIF in e.g.
CC hepatocytes, neurons and leukocytes. This clone comprises the full
CC length human LIFR.
XX SQ Sequence 1097 AA;

Query Match 8.1%; Score 277; DB 15; Length 1097;
Best Local Similarity 21.7%; Pred. No. 2.5e-13;
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

QY 27 PHGSGPLQCYSGVPLGILNCSEWP-----LGDLETPPVLYHQ-SQKYPNRRVWEVKVP 79
DB 332 pbdtpqqlnc-ethdikelicwmpgrvtalvgpratsylvesfsgky--vrikraesp 388
QY 80 SKQSW-----VTIPREQ---FTMADKLLIWGTQKGRPL---WSSVSYNLETKMPDPTPQIF 129
DB 389 tnesyqlfqlmpnqelnyftl-----nahpigrsqstlilvnitekvyphptstf 439
QY 130 SQVDISEATLEATVQWAPVVPFQKALTCQRYKCOAEAWTRLEPQLKTDGLRP---- 185
DB 440 kvkdnsta---vkswhlpgnfakinficeleikksns---vqeqrnvtikgvenssly 493
QY 186 VEMQNEPCTCYQVSGRCOVENGYPWGEWSPLSFOTPFELDPE---DVWVSGTVCTSGK 242
DB 494 valdklnpyltyfrircstetfkwskwnkqhltteaspskpdwtrews---sdgk 550
QY 243 RAALLVWKDPRPCVQ-----VITYTFWFGADITTTQEEVPCCKSPVPANME-----WAVY 292
DB 551 n-lllywk-plpineangkilyynvscsdeetqslseipdpqhkaeirlkndyilsvv 608
QY 293 SPGNSTSVVPTNLSVLCLAPESAPCDVGVSSADG-SPGIKVTWKQGTGRKPLEYVVDNAQ 351
DB 609 ak-navgssppsakia-----smipnddkieqvvgmgkgillitwhypmtcdyvikwcn 663
QY 352 DGDSDLK-LNWRLLPPGNLSTLLPG-EFKGGVGPYRTTAVYSGGLAAAPSVMGPREELV 409
DB 664 srspeclmdwkrkvpnstetviesdefrpgirynfflygcnrqgyqlrsmlyieela 723

QY 410 PLAGPAVRLPDDPCTPVVAMGEVPRHQLRGQATHYF-----CIQSRGLS 456
DB 724 pivapn-ftvedtsadsilvkwedipveelrgflrylvyfgkgerdtskmrvlesgrsd 782
QY 457 TVCRNVSSQTO-TATLPNLH-SGSFKLWTVTVSVAGGPPGDPOLSLHL--PDNRIRKAL 512
DB 783 ikvknitdisqktrlriadiqgktsyhlvrayt---dggvgpeksmvvyvtckensv----- 834
QY 513 PWFLSLWGLL-----LMCGCLSLASTRCLOARCLHWRHKLLOPWIER-----VP 557
DB 835 -----gllailpavavivgv---vtsllycykr-----ewiketfypdip 874
QY 558 DPANSNS-----GQPIKEVSL-PQPKDGPILP-----VEVEF-LQPVVESP 599
DB 875 npenckalgfqksvcegssalktlempctpnnnevletrsafpkiedtelispvaerpe 934

RESULT 14
AAR74097
ID AAR74097 standard; Protein; 1097 AA.
AC AAR74097;
XX AAR74097;
DT 22-JAN-1996 (first entry)
XX Human leukaemia inhibitory factor receptor (LIF-R).
DE Leukaemia inhibitory factor receptor; LIF-R; cachexia; human; murine;
KW atherosclerosis; obesity; bone disorder.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 1..44
FT /note= "signal peptide"
FT Protein 45..1097
FT /note= "mature protein - claim 1"
FT Modified-site 64
FT /note= "glycosylation site"
FT Modified-site 85
FT /note= "glycosylation site"
FT Modified-site 131
FT /note= "glycosylation site"
FT Modified-site 143
FT /note= "glycosylation site"
FT Modified-site 191
FT /note= "glycosylation site"
FT Modified-site 243
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FT Modified-site 303
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FT Modified-site 489
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FT Modified-site 572
FT /note= "glycosylation site"
FT Modified-site 652
FT /note= "glycosylation site"
FT Modified-site 663
FT /note= "glycosylation site"
FT Modified-site 680
FT /note= "glycosylation site"
FT Misc-difference 689
FT /note= "encoded by CAT"

FT Modified-site 729 /note= "glycosylation site"
 FT Modified-site 787 /note= "glycosylation site"
 FT Domain 834..859 /note= "transmembrane domain"
 FT Modified-site 1010 /note= "glycosylation site"
 FT US5420247-A.
 PN 30-MAY-1995.
 PD 13-DEC-1990; 90US-0626725.
 XX 11-SEP-1992; 92US-0943843.
 PR 13-DEC-1990; 90US-0626725.
 PR 13-MAR-1991; 91US-0670608.
 XX (IMMV) IMMUNEX CORP.
 PA Beckmann PM, Gearing DP;
 XX WPI: 1995-206309/27.
 DR N-PSDB; AAQ92272.
 XX
 XX New leukaemia inhibitory factor receptor proteins - useful for
 PT research, therapeutic and diagnostic purposes, esp. for the
 PT treatment of cancer associated cachexia
 PT
 PS Claim 1: Column 57-64; 47pp; English.
 XX
 XX This sequence represents human leukaemia inhibitory factor receptor
 CC (LIF-R). This sequence was encoded by the composite full length cDNA
 CC for human LIF-R. The cDNA sequence was isolated by screening human cDNA
 CC and genomic libraries with a probe derived from human clone 65 LIF-R
 CC cDNA. This receptor mediates LIF activity. LIF is a polypeptide hormone
 CC which acts on a variety of cells, and is highly conserved in a variety
 CC of species. LIF-R is present on the surface of a large number of
 CC hematopoietic and non-hematopoietic cells, including monocyte
 CC macrophages, megakaryocytes, osteoblasts and placental trophoblasts.
 CC The proteins represented by AAR74095-6 are also LIF-R proteins. These
 CC proteins are useful for research, where they can be used to study the
 CC structural and biological characteristics of native LIF-R. They are also
 CC useful for therapeutic purposes, e.g. to treat cachexia, atherosclerosis,
 CC obesity or bone disorders, and can be used for diagnostic purposes, e.g.
 CC for determination of LIF or diagnosis of diseases associated with
 CC abnormal LIF-R.
 XX
 S Sequence 1097 AA;
 Query Match 8.1%; Score 277; DB 16; Length 1097;
 Best Local Similarity 21.7%; Pred. No. 2,5e-13;
 Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;
 QY 27 PHGSPGLQCYGVGILNCWEP-----LGDLETPPVLYHQ-SQYHPNRVMEVKVP 79
 DB 332 pddtpqqlnc-ethdlkeilcswngprvtalvgpratsyltvesfsgky--vrikraeap 388
 QY 80 SKQSW----VTIPREQ---FTMADKLLIWGTQGRPL---WSSVSVNLETKMKTDPQIF 129
 DB 389 tnesyqlflgmnpqelynftl-----nahnplgrsgdtilvnitekyvphptstf 439
 QY 130 SQVDISEATLEATVQWAPPWPQKALTCQFRVKEQAEAWTRLEPKLTDGLTP---- 185
 DB 440 kvkdinsta----vklswlpgnfakinfleieikns-----vdeqrnvtikgvenssyl 493
 QY 186 VEMONLEPGTCYQVSGQCVENGYPWGEWSSPLSFQTFPFLDPE---DWVSGTVCEISGK 242
 DB 494 valdklapytlytfricrstetfkwskwnkqhlteaspskpdtrws---sdgk 550
 QY 243 RAALLVWKDRPCVQ-----VTTYTWFGAGDITTTQEBVPCCKSPVPANMBE-----NAWV 292

DB 551 n-liiywk-plpineangkilsynvscsdeetqtsiseipdqghkaeifrlkndyisvv 608
 QY 293 SPGNSTSVPPPTNLISVLAPESAPCDGVSSADG-SPGKVTWKQTRKPLEYVVDWAQ 351
 DB 609 ak-nsvgsppskia-----smelpnddikiqevvgmgkgllltwhydpmtcdyvikwn 663
 QY 352 DGDSDLKL-NWTRLPPGNLSTLLPG-EFKGGVPIRYITVAVYSGGLAAAPSVMGFPREELV 409
 DB 664 srssepclmdwrkvpnsstetviesdefrgirynfflygcrnqgqllrsmigyleela 723
 QY 410 PLAGPAVWRLPDDPGTPVWAVEPRHQLRGQAHYTF-----CIGRGLS 456
 DB 724 pivapn-ftvedtsadslivkwedipvealrgflgyfkgxerdtakmrvesgrsd 782
 QY 457 TVCRNVSSQTO-TATLPNLH-SGSFKLWTVSTVAGOGPPGPDLSLHL--PDNRIRWKAL 512
 DB 783 lkvknitdisqkltliadiqgktsyhlvirayt---dggvgpeksmyvvtkensv----- 834
 QY 513 PMFLSLWGLL-----LMGCGLSLASTRCLOARCLHWRHKLKPQWIWER-----VP 557
 DB 835 -----gliitailipvavavivgv---vtsilcykr-----ewiketfypdip 874
 QY 558 DPANSNS-----GOPYIKEVSL-POPPKDGPILE-----VEEVE-LQPVVESP 599
 DB 875 npenckalqfksvcegsalktlempcpnvnveletrsafpkiedteifspvaerpe 934
 RESULT 15
 AAR45774
 ID AAR45774 standard; Protein; 1001 AA.
 XX
 AC AAR45774;
 XX
 DT 04-AUG-1994 (first entry)
 XX
 DE Human leukaemia inhibitory factor receptor (clone hulifr.65).
 XX
 KW Leukaemia inhibitory factor receptor; LIFR; LIF; therapy;
 KW diagnosis; assay; antibodies; inhibition; cachexia;
 KW atherosclerosis; obesity; bone; calcium; metabolism.
 XX
 OS Homo sapiens.
 XX
 PN US5284755-A.
 XX
 PD 08-FEB-1994.
 XX
 PF 13-DEC-1990; 90US-0626725.
 XX
 PR 13-DEC-1990; 90US-0626725.
 PR 13-MAR-1991; 91US-0670608.
 PR 11-SEP-1992; 92US-0943843.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Beckmann MP, Gearing DP;
 XX
 DR WPI: 1994-056341/07.
 DR N-PSDB; AAQ55940.
 XX
 PT DNA encoding leukaemia inhibitory factor receptor - esp. soluble
 PT receptor, used as competitive inhibitor of LIF binding to cell
 PT surface, in therapy, diagnosis and assays
 XX
 PS Claim 1: Column 42-48; 44pp; English.
 XX
 CC Soluble forms of the leukaemia inhibitory factor receptor (LIFR)
 CC having the transmembrane domain deleted can be used in therapy,
 CC diagnosis, in assays for LIF or LIFR, or for raising antibodies to
 CC LIFR. Soluble LIFR proteins can be used for competitive inhibition
 CC of binding of LIF to cell surface receptors. Conditions which could
 CC benefit from such inhibition include LIF-induced cachexia in cancer

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OM protein - protein search, using sw model

Run on: May 9, 2002, 06:04:24 ; Search time 24.01 Seconds
(without alignments)
583.905 Million cell updates/sec

Title: US-09-692-504-2
Perfect score: 3424
Sequence: 1 MNRLRVARLTPELLLSLMS.....IYSGYEKHFPTPEELGLLV 623

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues
number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3424	100.0	623	1	US-08-653-740-7
2	3424	100.0	623	2	US-09-073-594-7
3	3424	100.0	623	3	US-09-275-925-7
4	2044	59.7	636	1	US-08-653-740-5
5	2044	59.7	636	2	US-09-073-594-5
6	2044	59.7	636	3	US-09-275-925-5
7	1866.5	54.5	578	1	US-08-653-740-3
8	1866.5	54.5	578	2	US-09-073-594-3
9	1866.5	54.5	578	3	US-09-275-925-3
10	384	11.2	862	2	US-08-685-118-2
11	384	11.2	862	2	US-08-915-495-2
12	384	11.2	862	2	US-08-914-520-2
13	277	8.1	1001	2	US-08-419-652-7
14	277	8.1	1001	1	US-07-797-556-6
15	277	8.1	1001	1	US-07-943-843-2
16	277	8.1	1001	1	US-08-347-003-2
17	277	8.1	1097	1	US-07-943-843-6
18	277	8.1	1097	1	US-08-347-003-6
19	270	7.9	708	1	US-07-797-556-2
20	270	7.9	708	1	US-08-308-881-2
21	270	7.9	708	1	US-09-058-263-2
22	270	7.9	708	2	US-09-059-099-2
23	270	7.9	708	3	US-09-058-264-2
24	270	7.9	708	5	PCT-US95-06530-2
25	264	7.7	918	2	US-08-825-558-6
26	261	7.6	602	2	US-08-419-652-6
27	261	7.6	783	6	5422248-2

28	261	7.6	836	1	US-07-923-976-4	Sequence 4, Appl1
29	255.5	7.5	837	1	US-07-923-976-2	Sequence 2, Appl1
30	253	7.4	572	2	US-08-419-652-5	Sequence 5, Appl1
31	253	7.4	863	1	US-07-923-976-8	Sequence 8, Appl1
32	228	6.7	771	1	US-07-923-976-6	Sequence 6, Appl1
33	226	6.6	658	2	US-08-825-558-4	Sequence 4, Appl1
34	193.5	5.7	979	1	US-08-308-881-6	Sequence 6, Appl1
35	193.5	5.7	979	2	US-09-058-263-6	Sequence 6, Appl1
36	193.5	5.7	979	3	US-09-059-099-6	Sequence 6, Appl1
37	193.5	5.7	979	3	US-09-058-264-6	Sequence 6, Appl1
38	193.5	5.7	979	5	PCT-US95-06530-6	Sequence 6, Appl1
39	176.5	5.2	719	1	US-07-943-843-4	Sequence 4, Appl1
40	176.5	5.2	719	1	US-08-347-003-4	Sequence 4, Appl1
41	175	5.1	488	2	US-08-599-455B-5	Sequence 5, Appl1
42	175	5.1	488	4	US-09-069-781B-5	Sequence 5, Appl1
43	153	4.5	894	2	US-08-599-455B-2	Sequence 2, Appl1
44	153	4.5	894	4	US-09-069-781B-2	Sequence 2, Appl1
45	153	4.5	896	2	US-08-640-389A-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1
US-08-653-740-7
; Sequence 7, Application US/08653740
; Patent No. 5792850
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,740
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-653-740-7

Query Match 100.0%; Score 3424; DB 1; Length 623;
Best Local Similarity 100.0%; Pred. No. 3e-292;
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNRLRVARLTPELLLSLMSLLGTRPHGSPGLOCYSVGPLGILNCSEWPLGLDLETPPV 60
Db 1 MNRLRVARLTPELLLSLMSLLGTRPHGSPGLOCYSVGPLGILNCSEWPLGLDLETPPV 60

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-594-7

Query Match 100.0%; Score 3424; DB 2; Length 623;
Best Local Similarity 100.0%; Pred. No. 3e-292;
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 LXHSQKYPHNRWVKVPSKOSWVTIPREQFTMDKLLIWTGKGRPLWSSVSVNLEQ 120
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|
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Db 61 LXHSQKYPHNRWVKVPSKOSWVTIPREQFTMDKLLIWTGKGRPLWSSVSVNLEQ 120
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|
|
QY 121 MKPDTPIQSVDISEATLEATVQAPVWPQKALTCQFYKECOAEAWTRLEPQKLT 180
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|
|
Db 121 MKPDTPIQSVDISEATLEATVQAPVWPQKALTCQFYKECOAEAWTRLEPQKLT 180
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|
|
QY 181 DGLTPVEMONLPGTCYQVSGRCQVNGYPMGEWSSPLSFOTPFDPEDVWVSGTVCETS 240
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|
|
Db 181 DGLTPVEMONLPGTCYQVSGRCQVNGYPMGEWSSPLSFOTPFDPEDVWVSGTVCETS 240
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|
|
QY 241 GKRAALLVWKDRPCQVQVTVYTFVFGAGDITTTQEEVPCCKSPVPAMWNAVSPGNSTSW 300
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Db 241 GKRAALLVWKDRPCQVQVTVYTFVFGAGDITTTQEEVPCCKSPVPAMWNAVSPGNSTSW 300
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|
|
QY 301 VPPTNLSLVCLAPESAPCDVGVSSADGSPGKIVTWKQGRKPLEYVVDNAQDGSDDLKLN 360
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Db 301 VPPTNLSLVCLAPESAPCDVGVSSADGSPGKIVTWKQGRKPLEYVVDNAQDGSDDLKLN 360
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|
|
QY 361 WTRLPNGLSTLLPGEFKGGVPIRITVTAVYSGGLAAAPSVMGFREELVPLAGPAWRLP 420
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|
|
Db 361 WTRLPNGLSTLLPGEFKGGVPIRITVTAVYSGGLAAAPSVMGFREELVPLAGPAWRLP 420
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|
|
QY 421 DDPGTPVYVWAVEVPRHQLRGQATHYTFCIQSRGLSTVCRNVSSQTQTATLPLNLSHGSSEK 480
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|
|
Db 421 DDPGTPVYVWAVEVPRHQLRGQATHYTFCIQSRGLSTVCRNVSSQTQTATLPLNLSHGSSEK 480
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|
|
QY 481 LWVTYSTVAGQPPGPDLSLHLPDNRIRWKALPWFLSLWGLLLMGCGLSLSTRCLQARC 540
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|
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Db 481 LWVTYSTVAGQPPGPDLSLHLPDNRIRWKALPWFLSLWGLLLMGCGLSLSTRCLQARC 540
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|
|
QY 541 LHWHRKLLPQWIERVDPDPANNSGOPYIKEVSLPQPKDGPILVEEVELOPVVESPKA 600
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|
|
Db 541 LHWHRKLLPQWIERVDPDPANNSGOPYIKEVSLPQPKDGPILVEEVELOPVVESPKA 600
|
|
|
QY 601 SAPIYSGYKHEFLPTPEELGLLV 623
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Db 601 SAPIYSGYKHEFLPTPEELGLLV 623
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|
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RESULT 2
US-09-073-594-7
; Sequence 7, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: zymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073.594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31

```

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-594-7

Query Match 100.0%; Score 3424; DB 2; Length 623;
Best Local Similarity 100.0%; Pred. No. 3e-292;
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRRLVARLTPILELLLSLMSLLLGTRPHGSPGLQCYSGVPLGILNCSWEPLDLETPPV 60
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Db 1 MNRRLVARLTPILELLLSLMSLLLGTRPHGSPGLQCYSGVPLGILNCSWEPLDLETPPV 60
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QY 61 LXHSQKYPHNRWVKVPSKOSWVTIPREQFTMDKLLIWTGKGRPLWSSVSVNLEQ 120
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|
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Db 61 LXHSQKYPHNRWVKVPSKOSWVTIPREQFTMDKLLIWTGKGRPLWSSVSVNLEQ 120
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QY 121 MKPDTPIQSVDISEATLEATVQAPVWPQKALTCQFYKECOAEAWTRLEPQKLT 180
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Db 121 MKPDTPIQSVDISEATLEATVQAPVWPQKALTCQFYKECOAEAWTRLEPQKLT 180
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QY 181 DGLTPVEMONLPGTCYQVSGRCQVNGYPMGEWSSPLSFOTPFDPEDVWVSGTVCETS 240
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Db 181 DGLTPVEMONLPGTCYQVSGRCQVNGYPMGEWSSPLSFOTPFDPEDVWVSGTVCETS 240
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|
QY 241 GKRAALLVWKDRPCQVQVTVYTFVFGAGDITTTQEEVPCCKSPVPAMWNAVSPGNSTSW 300
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Db 241 GKRAALLVWKDRPCQVQVTVYTFVFGAGDITTTQEEVPCCKSPVPAMWNAVSPGNSTSW 300
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|
QY 301 VPPTNLSLVCLAPESAPCDVGVSSADGSPGKIVTWKQGRKPLEYVVDNAQDGSDDLKLN 360
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|
|
Db 301 VPPTNLSLVCLAPESAPCDVGVSSADGSPGKIVTWKQGRKPLEYVVDNAQDGSDDLKLN 360
|
|
|
QY 361 WTRLPNGLSTLLPGEFKGGVPIRITVTAVYSGGLAAAPSVMGFREELVPLAGPAWRLP 420
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Db 361 WTRLPNGLSTLLPGEFKGGVPIRITVTAVYSGGLAAAPSVMGFREELVPLAGPAWRLP 420
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QY 421 DDPGTPVYVWAVEVPRHQLRGQATHYTFCIQSRGLSTVCRNVSSQTQTATLPLNLSHGSSEK 480
|
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Db 421 DDPGTPVYVWAVEVPRHQLRGQATHYTFCIQSRGLSTVCRNVSSQTQTATLPLNLSHGSSEK 480
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|
QY 481 LWVTYSTVAGQPPGPDLSLHLPDNRIRWKALPWFLSLWGLLLMGCGLSLSTRCLQARC 540
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Db 481 LWVTYSTVAGQPPGPDLSLHLPDNRIRWKALPWFLSLWGLLLMGCGLSLSTRCLQARC 540
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|
|
QY 541 LHWHRKLLPQWIERVDPDPANNSGOPYIKEVSLPQPKDGPILVEEVELOPVVESPKA 600
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|
|
Db 541 LHWHRKLLPQWIERVDPDPANNSGOPYIKEVSLPQPKDGPILVEEVELOPVVESPKA 600
|
|
|
QY 601 SAPIYSGYKHEFLPTPEELGLLV 623
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Db 601 SAPIYSGYKHEFLPTPEELGLLV 623
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|
|

RESULT 3
US-09-275-925-7
; Sequence 7, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:

```


ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 623 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-275-925-7

Query Match 100.0%; Score 3424; DB 3; Length 623;
Best Local Similarity 100.0%; Pred. No. 3e-292;
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRRLVRLTPELLLSMSLLGTRPHGSPGLQCYSGVPLGILNCSWEPLGDLTPPV 60
DB 1 MNRRLVRLTPELLLSMSLLGTRPHGSPGLQCYSGVPLGILNCSWEPLGDLTPPV 60
QY 61 LYHQSKYHPNRVWVKVPSKQSWTIPREQFTMDKLLINGTQKGRPLWSSVSNLETO 120
DB 61 LYHQSKYHPNRVWVKVPSKQSWTIPREQFTMDKLLINGTQKGRPLWSSVSNLETO 120
QY 121 MKPDPQIFSQVDISEATLEATVQWAPPVMPPOKALTCQFRYKCEQAEAWTRLEPQKT 180
DB 121 MKPDPQIFSQVDISEATLEATVQWAPPVMPPOKALTCQFRYKCEQAEAWTRLEPQKT 180
QY 181 DGLTPVENQNLPGTCYQVSGRCQVNGYPMGWSPLSFQTPFLDPEDVWVSGTVCTS 240
DB 181 DGLTPVENQNLPGTCYQVSGRCQVNGYPMGWSPLSFQTPFLDPEDVWVSGTVCTS 240
QY 241 GKRAALLVWKDPRPCVQVYTWFGAGDITTTQEEVPCKSPVPAMWAVVSPGNSTSW 300
DB 241 GKRAALLVWKDPRPCVQVYTWFGAGDITTTQEEVPCKSPVPAMWAVVSPGNSTSW 300
QY 301 VPPTNLSLVCLAPESAPCDVGVSSADGSPGKVTWKQGRKPLEYVVDWAQDGLDKLN 360
DB 301 VPPTNLSLVCLAPESAPCDVGVSSADGSPGKVTWKQGRKPLEYVVDWAQDGLDKLN 360
QY 361 WTRLPNGNLSTLLPGEFGVGYRITVAVYSGGLAAAPSVWGFREELVPLAGPAWRLP 420
DB 361 WTRLPNGNLSTLLPGEFGVGYRITVAVYSGGLAAAPSVWGFREELVPLAGPAWRLP 420
QY 421 DPPGCTPVVWAGEVPRHQLRGQATHVTFICQSRGLSTVCRNVSSOTQATLPLNLSGSEK 480
DB 421 DPPGCTPVVWAGEVPRHQLRGQATHVTFICQSRGLSTVCRNVSSOTQATLPLNLSGSEK 480
QY 481 LWVTVSTVAGQPPGDLNLRIRWALPWFSLWGLLMLGCLSLASTRCLQARC 540
DB 481 LWVTVSTVAGQPPGDLNLRIRWALPWFSLWGLLMLGCLSLASTRCLQARC 540
QY 541 LHWHRKLLPQWIERVDPDANSNGQPIKEVSLPQPKDGPILVEVEVELOPVVSPKA 600
DB 541 LHWHRKLLPQWIERVDPDANSNGQPIKEVSLPQPKDGPILVEVEVELOPVVSPKA 600

DB 541 LHWHRKLLPQWIERVDPDANSNGQPIKEVSLPQPKDGPILVEVEVELOPVVSPKA 600
QY 601 SAPIYSGYEKHEFLPTPEELGLLV 623
DB 601 SAPIYSGYEKHEFLPTPEELGLLV 623
RESULT 4
US-08-653-740-5
Sequence 5, Application US/08653740
Patent No. 5792850
GENERAL INFORMATION:
APPLICANT: James W. Baumgartner
APPLICANT: Donald C. Foster
APPLICANT: Frank J. Grant
APPLICANT: Cindy A. Sprecher
TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,740
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 95-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-740-5

Query Match 59.7%; Score 2044; DB 1; Length 636;
Best Local Similarity 62.8%; Pred. No. 4.4e-171;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

QY 9 LTPLELLLSMSLLGTRPHGSPGLQCYSGVPLGILNCSWEPLGDLTPPVLYHQSKY 68
DB 14 LPKALLPLWLLFQTRPQSGAGPLQCYGVGPLGILNCSWEPLGDLGAPSLHLSQKY 73
QY 69 HPNRVWVKVPSKQSWTIPREQFTMDKLLINGTQKGRPLWSSVSNLETOKPDTPQI 128
DB 74 RSNKTQTVAAAGRSWAIPREQFTMSDKLLYMGTRKAGPLPPVFNLETOKPNAPRL 133
QY 129 FSQVDISEATLEATVQWAPPVMPPOKALTCQFRYKCEQAEAWTRLEPOLKTDGLTPVEM 188
DB 134 GPDVDFSEDDPLEAVVHWAPPTWPSHKVLICQFHFRRCQEAATWLEPELKTIPTPVEI 193
QY 189 QNLEPGTCYQVSGRCQVNGYPMGWSPLSFQTPFLDPEDVWVSGTVCTSGKRAALL 247
DB 194 ODLELATGYKVVYGRCRMEKEEDLWGENSPILSFQTPPSAPKDVWVSGNLGTPGGEPL 253
QY 248 WVKDPRPCVQVYTWFGAGDITTTQEEVPCKSPVPAMWAVVSPGNSTSWPPTNL 307
DB 254 LWKAPGPCVQVSYKVMFWVWVGRGELSPGEGITCCSLIPSGAEWARYSAVNATSWEPNL 313

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QY 308 LVCLAPESAPCDVGVSSADSGPGIKVTKQGRKPLEYVVDWAQDGLDKLNWRLPPG 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 LVCLDSASAPRSVAVSSIAAGSTELLVTWQPGCEPLEHVVDWARDGDPLEKLNWRLPPG 373
QY 368 NLSTLLPGEFGKGVPRITVTAVYSGGLAAPSVWGFREELVPLAGVAVWRLPDDPPGTP 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 374 NLSALLPGNFTVGVPRITVTAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPPGP 433
QY 428 VWAVEVPRHQLRGOATHYTCIQSRGLSTVCRNVSSOTATLPLNLHSGSEFKLWTVST 487
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Db 434 AIANGVPRHQLRGLHLYTLCAQSGTSPSCMVNSGNTQSVTLPLPWGPCELWTVST 493
QY 488 VAGCGPPGDLSLHLPDNRIRKALPMFLSLWGLLLMGCGLSLSTRCLQARCLHWRHKL 547
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Db 494 IAGCGPPGPTLRLHLPDNTLRKVLPGILFLWGLFLGLCGGLSLATS- ---GRCYHLRHKV 549
QY 548 LPQWIWVRVDDPANSSGOPYIKEYSLPQPPKGPPILEVEEVELOQPWVES- ---PKASAPI 604
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 550 LPRWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPPVPMESSQPAQATAPL 609
QY 605 YSGYKHFLLPTPEELGLL 622
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Db 610 DSGYKHFLLPTPEELGLL 627

RESULT 5
US-09-073-594-5
; Sequence 5, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-073-594-5
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Query Match 59.7%; Score 2044; DB 2; Length 636;
Best Local Similarity 62.8%; Pred. No. 4 4e-171;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

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QY 9 LTPLELLLSLMSLLGLTRPHGSPGLQCYSVGPIGLINCSWEPLDGLTTPVLYHSQKY 68
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Db 14 LPKLALLPLLLWVLFQRTROGSAGPLQCYGVGPIGLDGLNCSWEPLDGLGAPSELHLSQKY 73
QY 69 HPRNVEVVKVPSKQSVVTPREOFTWADKLLIWGTOGRPLWSSVSVNLETQMKPDTQPI 128
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Db 74 RSNKTTVAVAAGRSVAIPREQLTMSDKLLVWGTAGOPPLWPPVFNLETQMKPNAPRL 133
QY 129 FSOVDISEATLEATVQAWPPKALTCQFRYKCEQAEAWTRLEPOLKTLDTLPVEM 188
    :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 134 GPDVDESDPLEATVHWAPPTWPSHKVLCQFHYRRCQAEAWTRLEPELKTPLTPVEI 193
QY 189 QNLEPTCYQVSGRCQVENGYP- WGEWSSPLSFQTPPLPEDVWVSGTVCETSGKRAALL 247
    :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 194 QDLELATKYVGRCRMEKEEDLWGSPLTSFQTPPSAPKDVWVSGNLCGTPGGBEPLL 253
QY 248 VWKDPKPCQVQVTVVWFGAGDITTTQEEVPCCKSPVPANMEWAVVSPGNSTSHVPTNLS 307
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Db 254 LMKAPGPCVQVSYKVMFWVGGRELSPEGITCCCLIPSGAEWARVSAVNATSWEPITNLS 313
QY 308 LVCLAPESAPCDVGVSSADSGPGIKVTKQGRKPLEYVVDWAQDGLDKLNWRLPPG 367
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Db 314 LVCLDSASAPRSVAVSSIAAGSTELLVTWQPGCEPLEHVVDWARDGDPLEKLNWRLPPG 373
QY 368 NLSTLLPGEFGKGVPRITVTAVYSGGLAAPSVWGFREELVPLAGVAVWRLPDDPPGTP 427
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Db 374 NLSALLPGNFTVGVPRITVTAVSASGLASASSVWGFREELAPLVGPTLWRLQDAPPGP 433
QY 428 VWAVEVPRHQLRGOATHYTCIQSRGLSTVCRNVSSOTATLPLNLHSGSEFKLWTVST 487
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Db 434 AIANGVPRHQLRGLHLYTLCAQSGTSPSCMVNSGNTQSVTLPLPWGPCELWTVST 493
QY 488 VAGCGPPGDLSLHLPDNRIRKALPMFLSLWGLLLMGCGLSLSTRCLQARCLHWRHKL 547
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Db 494 IAGCGPPGPTLRLHLPDNTLRKVLPGILFLWGLFLGLCGGLSLATS- ---GRCYHLRHKV 549
QY 548 LPQWIWVRVDDPANSSGOPYIKEYSLPQPPKGPPILEVEEVELOQPWVES- ---PKASAPI 604
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 550 LPRWWEKVPDPANSSGQPHMEQVPEAQPLGDLPILEVEEMEPPVPMESSQPAQATAPL 609
QY 605 YSGYKHFLLPTPEELGLL 622
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Db 610 DSGYKHFLLPTPEELGLL 627

RESULT 6
US-09-275-925-5
; Sequence 5, Application US/09275925
; Patent No. 6080406
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-073-594-5
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; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-275-925-5

Query Match          59.7%; Score 2044; DB 3; Length 636;
Best Local Similarity 62.8%; Pred. No. 4.4e-171;
Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 9 LTPLELLLSMLLGTGRPHGSPGLQCYSGVPLGILNCSWEPLDGLTPPVLYHQSKY 68
14 LPKALLPLLVLFQTRPQGSAGPLQCYGVPLGDLNCSWEPLDGLGAPSELHLSQSKY 73
Qy 69 HPNRVWEVKVPSQSWVTIPREQFTMAKLLIWGTQKGRPLWSSVSNLETKMPPDPTQI 128
Db 74 RSNKQTQVAVAGRSWAIPRQLTMSDKLLVWGTAKGQPLWPPVFVNLETKMKNAPRL 133
Qy 129 FSOVDISEATELEATVQWAPPVWPQKALTCQFRYKCOAEAWTLEPOLKTDGLTPVEM 188
Db 134 GPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQEAATLLEPELKTIPTPVEI 193
Qy 189 QNLEPGTCYQVSGRCQVNGYP-WGEWSSPLSFQTFPDLDPEDVWYSGTVCETSGKRAALL 247
Db 194 QDELELATGYKVYGRCKMEKEEDLWGENSPILSFQTPPSAPKDVWYSGNLCTPGGEEPLL 253
Qy 248 VVKDPRPCVQVITYTWFGAGDITTTQEEVPCKSPVPAMWAWVSPGNSWPPPTNLS 307
Db 254 LKAPGPGCVQVSYKVMFWVGGRELSPGEGTCCCLIPSGAENARVSAVNATSWEPNLNLS 313
Qy 308 LVCLAPESAPCDVGVSSADGSPGKIVTWKQTRKPLEYVVDWAQDGLDKLNWTRLP 367
Db 314 LVCLDSASAPRSVAVSSTAGSTELLVTWQPGGEPLHVVDWARGDPLEKLNWTRLP 373
Qy 368 NLSTLLPGEFGKGVPIRYITVAVYSGGLAAAPSVNGFREELVPLAGPAWRLPDDPGTP 427
Db 374 NLALLPGENFTVGPYRITVAVSAGSLASASSVNGFREELAPLVGPTLWRLQDAPGTP 433
Qy 428 VVANGVPRHQLRGQATHYTCIQSRGLSTVCRNVSSQTQTATLNLHSGSKFLWTVYST 487
Db 434 AIANGVPRHQLRGHLTHYTLCAQSGTSPSCMVNYSNGTQSVTLTDLPMWPCLEWVTAST 493
Qy 488 VAGQPPGPDLSLHLPDNRIRKALPWFILWGLLGMCGSLASTRCLQARCLHWRHKL 547
Db 494 IAGQPPGPILRLHLPDNTLRWKLPLGILFLWGLFLGCGLSLATS-----GRCYHLRHKV 549
Qy 548 LPQWTERVDPDANSNGOPYIKEYSLPQPKDGPFILEVEEVELOPVVES---PKASAPI 604
Db 550 LPRWVWEKVPDPANSSGPHMEQVPEAQPLGDLFILEVEEEMPPVMESSQPAQATAPL 609
Qy 605 YSGYEKHFLLPTPEELGLL 622
Db 610 DSGYEKHFLLPTPEELGLL 627

```

RESULT 7

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US-08-653-740-3
; Sequence 3, Application US/08653740
; Patent No. 5792850
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher

```

```

; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,740
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-653-740-3

```

Query Match 54.5%; Score 1866.5; DB 1; Length 578;

Best Local Similarity 61.7%; Pred. No. 1.5e-155;

Matches 353; Conservative 53; Mismatches 153; Indels 13; Gaps 3;

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Qy 9 LTPLELLLSMLLGTGRPHGSPGLQCYSGVPLGILNCSWEPLDGLTPPVLYHQSKY 68
Db 14 LPKALLPLLVLFQTRPQGSAGPLQCYGVPLGDLNCSWEPLDGLGAPSELHLSQSKY 73
Qy 69 HPNRVWEVKVPSQSWVTIPREQFTMAKLLIWGTQKGRPLWSSVSNLETKMPPDPTQI 128
Db 74 RSNKQTQVAVAGRSWAIPRQLTMSDKLLVWGTAKGQPLWPPVFVNLETKMKNAPRL 133
Qy 129 FSOVDISEATELEATVQWAPPVWPQKALTCQFRYKCOAEAWTLEPOLKTDGLTPVEM 188
Db 134 GPDVDFSEDDPLEATVHWAPPTWPSHKVLICQFHYRRCQEAATLLEPELKTIPTPVEI 193
Qy 189 QNLEPGTCYQVSGRCQVNGYP-WGEWSSPLSFQTFPDLDPEDVWYSGTVCETSGKRAALL 247
Db 194 QDELELATGYKVYGRCKMEKEEDLWGENSPILSFQTPPSAPKDVWYSGNLCTPGGEEPLL 253
Qy 248 VVKDPRPCVQVITYTWFGAGDITTTQEEVPCKSPVPAMWAWVSPGNSWPPPTNLS 307
Db 254 LKAPGPGCVQVSYKVMFWVGGRELSPGEGTCCCLIPSGAENARVSAVNATSWEPNLNLS 313
Qy 308 LVCLAPESAPCDVGVSSADGSPGKIVTWKQTRKPLEYVVDWAQDGLDKLNWTRLP 367
Db 314 LVCLDSASAPRSVAVSSTAGSTELLVTWQPGGEPLHVVDWARGDPLEKLNWTRLP 373
Qy 368 NLSTLLPGEFGKGVPIRYITVAVYSGGLAAAPSVNGFREELVPLAGPAWRLPDDPGTP 427
Db 374 NLALLPGENFTVGPYRITVAVSAGSLASASSVNGFREELAPLVGPTLWRLQDAPGTP 433
Qy 428 VVANGVPRHQLRGQATHYTCIQSRGLSTVCRNVSSQTQTATLNLHSGSKFLWTVYST 487
Db 434 AIANGVPRHQLRGHLTHYTLCAQSGTSPSCMVNYSNGTQSVTLTDLPMWPCLEWVTAST 493
Qy 488 VAGQPPGPDLSLHLPDNRIRKALPWFILWGLLGMCGSLASTRCLQARCLHWRHKL 547
Db 494 IAGQPPGPILRLHLPDNTLRWKLPLGILFLWGLFLGCGLSLATS-----GRCYHLRHKV 549

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QY 548 LPQIWERVPDPANNSGQPPIKEVSLPQQPK 579
 ||-|-||-|||||:-||-|-||-|
Dd 550 LPRWYEKVPDPANSSSG-----LLGPGR 573

RESULT 8
US-09-073-594-3
; Sequence 3, Application US/09073594
; Patent No. 5925735
; GENERAL INFORMATION:
; APPLICANT: James W. Baumgartner
; APPLICANT: Donald C. Foster
; APPLICANT: Frank J. Grant
; APPLICANT: Cindy A. Sprecher
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,594
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 578 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-594-3

Try Match	54.5%	Score 1866.5;	DB 2;	Length 578;
Best Local Similarity	61.7%	Pred. No. 1.5e-155;		
Matches 353; Conservative	53;	Mismatches 153;	Indels 13;	Gaps 3;

Qy	9	LTPLELLLLSLMSLLLTGRRPHGSGPPLQCYSGVPLGLTNCWEPGLDLETTPPVLYHQSQKY	68
Db	14	LPKALLPLLLWLFQRTROGSGAGPLQCYGVGPLDGLNCWEPGLDGLGAPSELHLQSQKY	73
Qy	69	HPNRVMEVKVPSKQSWTTPREQTWMADKLLIWGTQKGRPLKSSVSVNLETKMKTPOI	128
Db	74	RSNKQTQVAAAGRSWAIPREQLTMSDKLLVWGTGAGQPLPPVFNLETKMKNAPRL	133
Qy	129	FSQVDTSEETLEATVOWAPPWPPOKALTCQPRYKEQCAEAWTRLEBPQLKTDGLTPVPM	188
Db	134	GPVDSEDDPLEATVHWAPPTWPSHKVLTCQPHYRCQEAATWLEPELKIPTLPVBI	193
Qy	189	QNLPGTCYQVSGRCOVENYCP-WGWSWSPLSFOTPLDPEDWVSCTVCETSGKRAALL	247
Db	194	QDLELATGYKYGRCRMEXEEDLNGWSPILSFOTPPSAKQVWVSGNLCCTPGGEEPLL	253
Qy	248	VWKDPRPCQVTVTVWFGAGDITTTQEEVPCCKSPVPAMHMAVYSPGNSTSWPPTNLUS	307
Db	254	LWRAPGCPQVSYKVWFWVGGREISPEGITCCCSLLTSPGAEARVYASAVNATSWEPITNLUS	313

Qy	308	LVCLAPSPACDVGVSADSGSPGKIVTWKGTGRKPLEYVVDWAQDGDSDLKLNWTRLPPG	367
Db	314	LVCLDSASPRSAVSSIAAGTELLVWQPGCEPLEHVVDWMDGDGPLEKLNWRLPPG	373
Qy	368	NLSLTLLPGEFGKGVPRITVTAVYSGGLAAAPSVMGFRLELVPLAGPAVMNRLPDDPGPT	427
Db	374	NLSALLPCNFTVGPYRITVTAVSASGLASASSVMGFRLELPLVGPTLHRLQDAPPGT	433
Qy	428	VVANGVPRHQLRGQATHYFCIQSRGLSTVCRNVSSQQTATPLNLSGSSFKLWTVYST	487
Db	434	AIANGVPRHQLRGHLTHYLCAQSGTSPSCVMNVSGNTQSVTLPLDLPWMPGCELWTVAST	493
Qy	488	VAGOGPCPOLSLHLPNRIRWKLWFLSGLWGLLMGCGSLASTFRCLOARCLHWRHKL	547
Db	494	IAGOGPCPIURLHLPLONTLRKWKVLPGLFLWGLFLMGCGLSLATS-----GRCYHLRHKV	549
Qy	548	LPQWIWVRPDPANSPNSGQPYIKVSLPQPPK	579
Db	550	LPRWWEKVRPDPANSSG-----LLGPRP	573

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RESULT          9
US-09-275-925-3
: Sequence 3, Application US/09275925
: Patent No. 6080406
: GENERAL INFORMATION:
: APPLICANT: James W. Baumgartner
: APPLICANT: Donald C. Foster
: APPLICANT: Frank J. Grant
: APPLICANT: Cindy A. Sprecher
: TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Zymogenetics, Inc.
: STREET: 1201 Eastlake Avenue East
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/275,925
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Parker, Gary E
: REGISTRATION NUMBER: 31,648
: REFERENCE/DOCKET NUMBER: 95-31
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-442-6673
: TELEFAX: 206-442-6678
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 578 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-275-925-3

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Query Match	54.5%	Score 1866.5;	DB 3;	Length 578;
Best Local Similarity	61.7%	pred. NO. 1.5e-155;		
Matches 353;	Conservative	53;	Mismatches 153;	Indels 13;
				Gaps 3

[illegible]

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; MOLECULE TYPE: protein
; US-08-685-118-2

Query Match      11.2%; Score 384; DB 2; Length 862;
Best Local Similarity 25.1%; Pred. No. 3.8e-25;
Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;

QY 5 RVARUTLELLLSLMSLLGTRPHSGPGPLOCYSYVGLGILNCSEPLGD--LETPPVLY 62
Db 102 KLACINSDEIQICGAEIFGVNAPE--QPONLSCIQGEQGTACTWGRDTHLYEYTLQ 160
QY 63 HQSQYHNRNVEVK-----VPSKOSWVTIPREQFTMDADKLLIMGTQGR 107
Db 161 LSGPK---NLTWQCKDIYCDYDFGINTPES-----PESNFTAKVTAV-----N 204
QY 108 PLWSSVSNLETKMPTDTPQFSQVDISEEATLEATVQWAPVWPP-----QXA----- 156
Db 205 SLGSSSL-----PSTFTFLDI-----VRPLPP-WDIRIKFKQKASVSRCFL 244
QY 157 -----LTCQFRYKECOAEAWTRLEPOLKTDGLTPVEMONLEPGTCV--QVSGRCOVE 206
Db 245 YWRDEGLVLLNRLVRPSNRLNWNV---VTKAKGRHDLDLKPEFTEYFQISKLHL 301
QY 207 NGYPMGEWSSPLSFQTFPLDPE---DVMVSGTVCTSGKRAALLVMK-----DPRPCV-- 256
Db 302 KG-SWSDNSESLRAQTPPEEPTGMLDVWYMKRHIDYSRQQLSLF-WKNLSVSEARGKILH 359
QY 257 -QVITYWFGAGDITTOEEVPCCKSPVPAMWEWAV-VSPGNSTSWPPTNLS--VCLA 312
Db 360 YQVTLQELTGKAMQNTITGHTSWTVTPRTGNWAVAVSAANSKSSSLPRTINIMNCEA 419
QY 313 PESAPCDVGVSSADSGPGIKVTWQGRKP---LEVYVDWAQ---DGDSDLKLNWRLPP 366
Db 420 GLLAPQVSANS-EGMDNLTWPPKDPKDPNAVQYVYVWEHLHGGDTQVPLMWLRSP 478
QY 367 NLSTLLPGEFKGVYRITVAVYSGGLAAAPSVMGFREELVPLAGPAVWRLPDDPFGT 426
Db 479 YNVSALISENIKSYICYEIRVVAL--SGDQGGCSSILGSKHKAPLSGPHINAITEE-KGS 536
QY 427 PVWAVEVPRHLRQOATHYTCIQSRGLSTVCRNVSSQTQTATLP-----NLH----- 475
Db 537 ILISWNSIPVQEQMGLLHYRIYKE-----RDSNSQQLCEIPYRVSONSHPINSLQ 589
QY 476 -SGSEFKVWTVSTVAGQPPGPDLSLHLPDNRIRKALPWLFLSLWGLLWGLSLASTR 534
Db 590 PRVTVLWMTALTAAAGESSHGNREFECL-QGKANWMAFVAPISICIAIIVWG-----IFSTH 644
QY 535 CLQARCLHWRHKLPLQWITWVRPDPANSPNSQPY-IKEVSLPQP-----PKDGP 583
Db 645 YFOQKVFVLLAALRPQWCSREIPDPANSTCAKYPVIAEKTQLDLRLIDWPTDEPPEP 704
QY 584 LEVEEV--ELQPVVESPKAS 601
Db 705 LVISEVLHQVTPVFRHPPCS 724

```

RESULT 11

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US-08-915-495-2
; Sequence 2, Application US/08915495
; Patent No. 5852176
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110

```

```

; MOLECULE TYPE: protein
; US-08-685-118-2

Query Match      11.2%; Score 384; DB 2; Length 862;
Best Local Similarity 25.1%; Pred. No. 3.8e-25;
Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;

QY 5 RVARUTLELLLSLMSLLGTRPHSGPGPLOCYSYVGLGILNCSEPLGD--LETPPVLY 62
Db 102 KLACINSDEIQICGAEIFGVNAPE--QPONLSCIQGEQGTACTWGRDTHLYEYTLQ 160
QY 63 HQSQYHNRNVEVK-----VPSKOSWVTIPREQFTMDADKLLIMGTQGR 107
Db 161 LSGPK---NLTWQCKDIYCDYDFGINTPES-----PESNFTAKVTAV-----N 204
QY 108 PLWSSVSNLETKMPTDTPQFSQVDISEEATLEATVQWAPVWPP-----QXA----- 156
Db 205 SLGSSSL-----PSTFTFLDI-----VRPLPP-WDIRIKFKQKASVSRCFL 244
QY 157 -----LTCQFRYKECOAEAWTRLEPOLKTDGLTPVEMONLEPGTCV--QVSGRCOVE 206
Db 245 YWRDEGLVLLNRLVRPSNRLNWNV---VTKAKGRHDLDLKPEFTEYFQISKLHL 301
QY 207 NGYPMGEWSSPLSFQTFPLDPE---DVMVSGTVCTSGKRAALLVMK-----DPRPCV-- 256
Db 302 KG-SWSDNSESLRAQTPPEEPTGMLDVWYMKRHIDYSRQQLSLF-WKNLSVSEARGKILH 359
QY 257 -QVITYWFGAGDITTOEEVPCCKSPVPAMWEWAV-VSPGNSTSWPPTNLS--VCLA 312
Db 360 YQVTLQELTGKAMQNTITGHTSWTVTPRTGNWAVAVSAANSKSSSLPRTINIMNCEA 419
QY 313 PESAPCDVGVSSADSGPGIKVTWQGRKP---LEVYVDWAQ---DGDSDLKLNWRLPP 366
Db 420 GLLAPQVSANS-EGMDNLTWPPKDPKDPNAVQYVYVWEHLHGGDTQVPLMWLRSP 478
QY 367 NLSTLLPGEFKGVYRITVAVYSGGLAAAPSVMGFREELVPLAGPAVWRLPDDPFGT 426
Db 479 YNVSALISENIKSYICYEIRVVAL--SGDQGGCSSILGSKHKAPLSGPHINAITEE-KGS 536
QY 427 PVWAVEVPRHLRQOATHYTCIQSRGLSTVCRNVSSQTQTATLP-----NLH----- 475
Db 537 ILISWNSIPVQEQMGLLHYRIYKE-----RDSNSQQLCEIPYRVSONSHPINSLQ 589
QY 476 -SGSEFKVWTVSTVAGQPPGPDLSLHLPDNRIRKALPWLFLSLWGLLWGLSLASTR 534
Db 590 PRVTVLWMTALTAAAGESSHGNREFECL-QGKANWMAFVAPISICIAIIVWG-----IFSTH 644
QY 535 CLQARCLHWRHKLPLQWITWVRPDPANSPNSQPY-IKEVSLPQP-----PKDGP 583
Db 645 YFOQKVFVLLAALRPQWCSREIPDPANSTCAKYPVIAEKTQLDLRLIDWPTDEPPEP 704
QY 584 LEVEEV--ELQPVVESPKAS 601
Db 705 LVISEVLHQVTPVFRHPPCS 724

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RESULT 10

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US-08-685-118-2
; Sequence 2, Application US/08685118
; Patent No. 5840530
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,118
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 862 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```


Query Match 8.1%; Score 277; DB 2; Length 620;
Best Local Similarity 21.7%; Pred. No. 5.8e-16;
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

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RESULT 14
US-07-797-556-6
Sequence 6, Application US/07797556
Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: Receptor for
TITLE OF INVENTION: Inhibitory
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street

```

RESULT 14
US-07-797-556-6

```

US-07-799-556-6
: Sequence 6, Application US/07797556
: Patent No. 5262522
: GENERAL INFORMATION:
: APPLICANT: Gearing, David P.
: TITLE OF INVENTION: Receptor for
: TITLE OF INVENTION: Inhibitory f
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Immunex Corporation
: STREET: 51 University Street

```

```

RESULT 13
US-08-419-652-7
; Sequence 7, Application US/08419652
; Patent No. 5831007
; GENERAL INFORMATION:
; APPLICANT: Chuva, Anne O
; APPLICANT: Gubler, Ulrich A
; TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110-1199
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.25

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RESULT 13
US-08-419-652-7
; Sequence 7, Application US/08419652
; Patent No. 5831007

GENERAL INFORMATION:
APPLICANT: Chua, Anne O
TITLE OF INVENTION: Gubler, Ulrich A
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Patent In Release #1.0.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,652
FILING DATE: 11-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,532
FILING DATE: 31-MAY-1994

; PRIOR APPLICATION DATA: ;
 ; APPLICATION NUMBER: US 08/094,713 ;
 ; FILING DATE: 19-JUL-1993 ;
 ; ATTORNEY/AGENT INFORMATION: ;
 ; NAME: Kass, Alan P ;
 ; REGISTRATION NUMBER: 32142 ;
 ; REFERENCE/DOCKET NUMBER: CD 9174 ;
 ; TELECOMMUNICATION INFORMATION: ;
 ; TELEPHONE: (201) 235-4205 ;
 ; TELEFAX: (201) 235-3500 ;
 ; INFORMATION FOR SEQ ID NO: 7: ;
 ; SEQUENCE CHARACTERISTICS: ;
 ; LENGTH: 620 amino acids ;

CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-6

Query Match 8.1%; Score 277; DB 1; Length 1001;
Best Local Similarity 21.7%; Pred. No. 1.2e-15;
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

QY 27 PHGSPGLOQYSGVGLILNCSEWEP-----LGDLETPPVLYHQ-SQKYHPNRVMEVKVP 79
DB 332 PPDTPQOLNC-ETHDLKEIICSNPGRVTLVGPRTATSYTLVESFGKY--VRLKRAEAP 388
QY 80 SKQSW-----VTIPREQ---FTMADKLLINGTQGRPL---WSSVSVNLETQMKPDPQIF 129
DB 389 TNEYSQLLFQMLPQNEIYNFTL-----NAHNPLGRSQSTILVNITEKVPYPTPTSF 439
QY 130 SQVDISEEATLEATVQWAPPVPPQKALTCQFPRYKCAQAEWTRLEPQLKTDLTP---- 185
DB 440 KVKDINSTA---VKLSMHLPGNFAKINFCEIEIKKNS---VQEQRNVTIKGVNSSYL 493
QY 186 VEMQNLPEPTCYQVSGRCQVNGYPMGWSPLSFOTPFLLDPE---DVMVSGTVCTETSGK 242
DB 494 VALDKLNPLYTYFRIRCSSTETETWKKSNKKQHLTTEASPSKGPDTWREWS---SDGK 550
QY 243 RAALLVWKDPRPCVQ-----VITYVWFGAGDITTTQEEVPCCKSPVPAMWE-----WAVV 292
DB 551 N-LIYYWK-PLPINEANGKILSYNVSCSSDEETQSLSEIPDPQHKAEIRLDKNDYIISV 608
QY 293 SPGNSTSWPPTNLSVLCLAPESAPCDVGVSSADG-SPGIKVTWKQGRKPLEYVVDWAQ 351
DB 609 AK-NSVGSPSPSKIA-----SMEIPNDLLKIEQVGMGKGIILLTWHYDPNMTCDYIKWCN 663
QY 352 DGDSDLKL-NWTRLPNGNLSTLPG-EFKGGVPYRITTVAVYSGGLAAAPSVMGPREELV 409
DB 664 SSRSECLMDWRKVPNSTETVIESDEFPRGIRYNFFLGCNRQNGQLLRSMIGYIEELA 723
QY 410 PLAGPAWRLPDDPGTPPVVANGVEPRHOLRGOATHYF-----CIGSRGLS 456
DB 724 PIVAPN-FTVEDTSADSLVKMEDIPVEELRGLFRLGYLFYFGKGERDTSKMRVLESGRSD 782
QY 457 TVCRNVSSOTO-TATLPNLH-SGSFKLWTVSTVAGQPPGPDLSLHL--PDNRIRWKL 512
DB 783 IKVKNITDISQKTLRIADLQGTSTHVLVRAVT---DGGVGPEKSPVYVTKNSV-----834
QY 513 PMFLSLWGLL-----LMGCGLSLSTRCLQARCLHRHKLLOWIWER-----VP 557
DB 835 -----GLIIALLIPVAVAVIGV---VTSILCYKKR-----EWIKETFPDIP 874

QY 558 DPANSNS-----GQPYIKIVSL-POPPKDGPILE-----VEEVE-LQPVVESP 599
DB 875 NPENCKALQFQKSVCGSSALKLTLENNPCTPNNVELETRSAPFKIEDTEIISVPAERPE 934
RESULT 15
US-07-943-843-2
Sequence 2, Application US/07943843
Patent No. 5284755
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Beckmann, M. P.
TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/943,843
FILING DATE: 19920911
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2606-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-943-843-2

Query Match 8.1%; Score 277; DB 1; Length 1001;
Best Local Similarity 21.7%; Pred. No. 1.2e-15;
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

QY 27 PHGSPGLOQYSGVGLILNCSEWEP-----LGDLETPPVLYHQ-SQKYHPNRVMEVKVP 79
DB 332 PPDTPQOLNC-ETHDLKEIICSNPGRVTLVGPRTATSYTLVESFGKY--VRLKRAEAP 388
QY 80 SKQSW-----VTIPREQ---FTMADKLLINGTQGRPL---WSSVSVNLETQMKPDPQIF 129
DB 389 TNEYSQLLFQMLPQNEIYNFTL-----NAHNPLGRSQSTILVNITEKVPYPTPTSF 439
QY 130 SQVDISEEATLEATVQWAPPVPPQKALTCQFPRYKCAQAEWTRLEPQLKTDLTP---- 185
DB 440 KVKDINSTA---VKLSMHLPGNFAKINFCEIEIKKNS---VQEQRNVTIKGVNSSYL 493
QY 186 VEMQNLPEPTCYQVSGRCQVNGYPMGWSPLSFOTPFLLDPE---DVMVSGTVCTETSGK 242
DB 494 VALDKLNPLYTYFRIRCSSTETETWKKSNKKQHLTTEASPSKGPDTWREWS---SDGK 550
QY 243 RAALLVWKDPRPCVQ-----VITYVWFGAGDITTTQEEVPCCKSPVPAMWE-----WAVV 292
DB 551 N-LIYYWK-PLPINEANGKILSYNVSCSSDEETQSLSEIPDPQHKAEIRLDKNDYIISV 608
QY 293 SPGNSTSWPPTNLSVLCLAPESAPCDVGVSSADG-SPGIKVTWKQGRKPLEYVVDWAQ 351
DB 609 AK-NSVGSPSPSKIA-----SMEIPNDLLKIEQVGMGKGIILLTWHYDPNMTCDYIKWCN 663

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